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OM protein - protein search, using sw model

Run on: May 27, 2003, 16:04:16 ; Search time 17 Seconds
(without alignments)
655.958 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVILLFLALCSAKPFTS.....PATRCVLRSVQLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

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5: /cgn2_6/ptodata/1/iaa/6CTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1799	90.3	373	4	US-09-724-864-43
2	1021	51.3	368	1	US-08-303-238-3
3	1021	51.3	368	4	US-08-458-834-3
4	1020	51.2	368	6	5340934-2
5	963.5	48.4	359	1	US-08-303-238-4
6	963.5	48.4	359	4	US-08-458-834-4
7	949	47.6	342	1	US-08-272-919-2
8	949	47.6	342	1	US-08-619-916-2
9	949	47.6	342	5	PCT-US95-08542-2
10	947	47.5	333	1	US-08-442-063A-27
11	907	45.5	353	6	5340934-4
12	847	42.5	307	1	US-08-442-063A-48
13	776	39.0	282	1	US-08-442-063A-45
14	616	30.9	236	1	US-08-442-063A-42
15	493	24.7	188	1	US-08-442-063A-39
16	384.5	19.3	141	1	US-08-442-063A-36
17	342.5	17.2	375	1	US-08-303-238-2
18	342.5	17.2	375	4	US-08-458-834-2
19	336	16.9	1525	3	US-09-191-647-2
20	336	16.9	1525	4	US-09-540-245A-2
21	336	16.9	1525	4	US-09-540-153-2
22	334.5	16.8	649	4	US-09-188-930-305
23	318	16.0	376	1	US-08-303-238-1
24	318	16.0	376	4	US-08-458-834-1
25	316	15.9	1480	3	US-09-191-647-7
26	316	15.9	1480	4	US-09-540-245A-7
27	316	15.9	1480	4	US-09-540-153-7

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173	100.5	5.0	456	2	US-08-910-731-2	Sequence 2, Appli	Sequence 2, Appli	246	91	4.6	1143	4	US-09-301-085-108	Sequence 108, App

247	91	4.6	1143	5	PCT-US95-04589-108	Sequence 108, App	320	85	4.3	853	4	US-08-913-880C-17	Sequence 17, Appl
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249	91	4.6	1144	1	US-08-261-663A-2	Sequence 4, Appli	322	85	4.3	860	4	US-08-913-880C-15	Sequence 15, Appl
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251	91	4.6	1144	3	US-09-357-206A-3	Sequence 3, Appli	324	85	4.3	865	4	US-08-913-880C-13	Sequence 13, Appl
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QY 232 TSVKGLPPTLLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANIPVR 291
Db 223 TSIPKDPSSITELSDYNNKISKVETEDIRYKNLQRLGLAFNQKYVENGSLANTPKIR 282
QY 292 EIHLENNKKIPSGLPKLYLQIIFLHNSSTARVGVNDFCPTVPKMKKSLYSALSLENN 351
Db 283 EIVLDNNRMRKVPGLUSSURYQVIFLHGKNLSSVGINDFCPIRADSKKNPYTGISLFAN 342
352 PVKYWEMQATFCVLSRMSVOLGNF 377
343 PVKYWAIQATFCVTRGRGVOLGNF 368

RESULT 2

Q9NXP3 ID Q9NXP3 PRELIMINARY; PRT; 187 AA.
AC Q9NXP3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CDNA FLJ20129 fis, clone COL06190.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000136; BAA90967.1; -;
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 3.
SQ SEQUENCE 187 AA; 21074 MW; BDBEE37373CA3DBE CRC64;

Query Match 48.6%; Score 968; DB 4; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.6e-61;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 MNALHVLMSANPLDNNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNNKI 252
Db 1 MNALHVLMSANPLDNNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNNKI 60
QY 253 STVELEDFKRYKELQRLGLGNKKITDIENGSLANIPVRRIHLENNKKIPSGLPKLY 312
Db 61 STVELEDFKRYKELQRLGLGNKKITDIENGSLANIPVRRIHLENNKKIPSGLPKLY 120
QY 313 LQIIFLHNSSTARVGVNDFCPTVPKMKKSLYSALSLENNPVKYWEMQATFCVLSRMSV 372
Db 121 LQIIFLHNSSTARVGVNDFCPTVPKMKKSLYSALSLENNPVKYWEMQATFCVLSRMSV 180
QY 373 QLGNFGM 379
Db 181 QLGNFGM 187

RESULT 3

Q9DE03 ID Q9DE03 PRELIMINARY; PRT; 359 AA.
AC Q9DE03;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Decorin
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'Nuigin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts."
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247822; AAG40157.1; -;
DR InterPro; IPR001611; LRR.
DR InterPro; IPR00372; LRR_Nterm.
DR InterPro; IPR003592; LRR_Out.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 7.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 3.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 7.
SQ SEQUENCE 359 AA; 39807 MW; F149F9AA4E7572C6 CRC64;

Query Match 47.7%; Score 950; DB 13; Length 359;

Best Local Similarity 50.8%; Pred. No. 6.7e-60;

Matches 189; Conservative 57; Mismatches 102; Indels 24; Gaps 4;

QY 7 LLFALCSAKPFPSFHIALKNMMLKDMEDTDDDDDDDDDDDDSLFPTREPRSHFF 66
Db 8 LLLVTACWALPFRQSGFL---DFMM-----EDEGSDVPTSPDP----- 44
QY 67 PFDLPFMPGFCQCYSRVVHCSDGLGTSVPTNIPFDTRMLDQNNKITEIKENDFKGLTS 126
Db 45 PVIGGPKCFRCQCHLRVQCSDLGLKAVPEDIPDDITLLDQNNKITEIKENDFKNLKG 104
QY 127 LVGLILNNKLTIKHPKAFLLTKKRLRYLSHNLQSEIPLNPKSLAELRIHENVKVKIQ 186
Db 105 LHALILVNNKLTIIHPKAFSPLTKLQRLYLSKNLLKEMPANMPKSLOELRIHENEITKIK 164
QY 187 KDTFKGMNALHVLMSANPLDNNNGIEPGAEGV-TVFIHIAEAKLTSVPKGLPPTLLEL 245
Db 165 KASFGNSHVIIVMELGSLNPLKTAGIEAGAFADLKRAVIRADTNITEVPGKLSLSEL 224
QY 246 HLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANIPVRRIHLENNKKIKTIPS 305
Db 225 HLDGNKIKTKLTADRLKGMKNLAKGLSYNQISSVENGTLSNAPHLRELHLDNNALTSVPP 284
QY 306 GLPELKYLQIIFLHNSSTARVGVNDFCPTVPKMKKSLYSALSLENNPVKYWEMQATFC 365
Db 285 GLPDHKYIQVYVHLHAHKAAGVTEDEFCPPGNTKKAMYSGLSLFSPNPVYEVQVPTFC 344
QY 366 VLRSMSVOLGNF 377
Db 345 VFDRSAIQNGNY 356

RESULT 4

Q9DDZ7 ID Q9DDZ7 PRELIMINARY; PRT; 410 AA.
AC Q9DDZ7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Biglycan-like protein 2.

RT	"Biglycan-like extracellular matrix genes of agnathans and teleosts."
RL	J. Mol. Evol. 51:363-373(2000).
DR	EMBL; AF247827; AAC40162.1; -.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000372; LRR_Nterm.
DR	InterPro; IPR003592; LRR_Out.
DR	InterPro; IPR003591; LRR_typ.
DR	Pfam; PF00560; LRR; 7.
DR	Pfam; PF01462; LRRNT; 1.
DR	SMART; SM00370; LRR; 4.
DR	SMART; SM00013; LRRNT; 1.
DR	SMART; SM00369; LRR_TYP; 8.
FT	NON_TER 1
SQ	SEQUENCE 310 AA; 34572 MW; 6FB8E05B14339EF5 CRC64;
Query Match 45.9%; Score 915; DB 13; Length 310; Best Local Similarity 56.2%; Pred. No. 1.7e-57; Matches 172; Conservative 51; Mismatches 81; Indels 2; Gaps	
QY	74 CPFGCCQSYRVVHCSDGLTSPVTNPFDTRMLDLQNKKIKEIKENDPKGLTSLYLGLIIN 133
DB	: :
DB	3 CPFGCCSARVOCSDGLGVSVFQAIPKQARDLDDLNKKITETKDQDFKGLNKLXALYL 62
QY	134 NKKLTTHPKAFATTKRLRLLYLSHNQLSEIPLNLPSLAELRIHENKVVKIOKDTFKGM 193
DB	: : : : :
DB	63 NNLSKVHPKAFAPLSSLDKLYISHNQLTEVPSCMPSSSLVELRIENNIKKIPKDAFSQM 122
QY	194 NALHVLMSANPDNNNGIEPGAEGV-TVPHIRIAAKLITSYPKGLPPTLLLEHLHDYNKI 252
DB	: : : :
DB	123 KRHALEMGNCPLOSTQEIVGAPEGLERLVVRVDSKLARIKPOLPNISIQELHLEHQI 182
QY	253 STVELEDKRYKELORLGIGNNKITDIENGSLANTIPRVEIHLENKCLKKIPSGLPKLKY 312
DB	: : : : :
DB	183 TALEQEDLIHYPIHRUGLSYNOIKVIQNSLETCHLRHLSDSNVLTQVPPGLAFLKH 242
QY	313 LQIFLHSNISARVGVDNFCPTVPKMKKSLYSALSILFNPNPVRYWEMQPATPRCVLSRMVS 372
DB	: : : :
DB	243 LQVVYLHSNKIAAVKSDDFCSGKGPRLVYSGISLFDPNVNYWDVPPSAFCVCVASRAV 302
QY	373 QLG-NF 377
DB	
DB	303 QFSQNF 308
RESULT 6	
Q9DE00	PRELIMINARY; PRT; 347 AA.
ID	Q9DE00
AC	Q9DE00;
CD	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	Biglycan-like protein 1 (Fragment).
GN	BGL1.
OS	Petromyzon marinus (Sea lamprey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC	Petromyzontiformes; Petromyzontidae; Petromyzon.
RN	NCBI_TaxID=7757;
OX	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=20496956; PubMed=11040287;
RX	Shintani S., Sato A., Toyosawa S., O'Huigin C., Klein J.;
RT	"Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL	J. Mol. Evol. 51:363-373(2000).
DR	EMBL; AF247825; AAC40160.1; -.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000372; LRR_Nterm.
DR	InterPro; IPR003592; LRR_Out.
DR	InterPro; IPR003591; LRR_typ.
DR	Pfam; PF00560; LRR; 8.
DR	Pfam; PF01462; LRRNT; 1.
DR	SMART; SM00370; LRR; 4.
DR	SMART; SM00013; LRRNT; 1.
DR	SMART; SM00369; LRR_TYP; 6.

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FT  NON_TER 1
SQ  SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;

Query Match 43.6%; Score 869.5; DB 13; Length 347;
Best Local Similarity 54.3%; Pred. No. 3.4e-54;
Matches 165; Conservative 54; Mismatches 84; Indels 1; Gaps 1;

QY 74 CPGGOCYSRVVHCSDGLTGSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 40 CPGGOCYSRVVHCSDGLTGSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILN 99
QY 134 NNLTKIHPKAPLTKKLRRLYLHNSQLSEIPLNLPKSLABELRIHENKVKKIQKDTFGM 193
DB 100 NNLTKIHPKAPAMVSLDKLYISHNRLTEVPTGTPPSLIELRVHENLKRVPKDTFINN 159
QY 194 NALHVLMSANPLDNNIGIEGAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNKI 252
DB 160 GOLHVIELGKPNLSSIEGAFNGLDKLTIRISYSLTQPKLPNSLLEHLEGNEI 219
QY 253 STVELEDFKRYKELQRLGIGNNKLTIDIEGSLANIPRVREIHLNENKLLKKTIPSGLPKLY 312
DB 220 VAIEDEDLFGYPYLFRLGLSYNNKITEVQNGSLAVSNGNRELHLDNNLLSVPPGLSKLRS 279
QY 313 LQITLHNSIARVGVNDFCPTVPKMKKSLXSAISLFFNPNVYKWEQMPATFRCVLSRMSV 372
DB 280 LNVVYLHNSNKEIVKPTDFCPTVPKRAQYAGISLYDNPVKYWEVPPSVFRCVHHNNAI 339
QY 373 QLGN 376
DB 340 HFGS 343

RESULT 7
Q9DDZ9 PRELIMINARY; PRT; 388 AA.
AC Q9DDZ9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Biglycan-like protein 1 (Fragment).
GN BGL1.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'huigin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL: AF247826; AAG40161.1; -.
ZFIN: ZDB-GENE-010102-1; dcn.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00560; LRR; 8.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00370; LRR; 4.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Typ; 7.
FT NON_TER 1
FT NON_TER 388 AA; 42542 MW; 2E07169E9B6071B CRC64;

Query Match 43.4%; Score 865.5; DB 13; Length 388;
Best Local Similarity 54.3%; Pred. No. 7.5e-54;
Matches 165; Conservative 53; Mismatches 85; Indels 1; Gaps 1;

QY 74 CPGGOCYSRVVHCSDGLTGSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILN 133
DB 81 CPGGOCYSRVVHCSDGLTGSVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILN 140
QY 134 NNLTKIHPKAPLTKKLRRLYLHNSQLSEIPLNLPKSLABELRIHENKVKKIQKDTFGM 193

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DB 141 NNLTKIHPKAPAMVSLDKLYISHNRLTEVPTGTPPSLIELRVHENLKRVPKDTFINN 200
QY 194 NALHVLMSANPLDNNIGIEGAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNKI 252
DB 201 GRUHVIELGKPNLSSIEGAFNGLDKLTIRISYSLTQPKLPNSLLEHLEGNEI 260
QY 253 STVELEDFKRYKELQRLGIGNNKLTIDIEGSLANIPRVREIHLNENKLLKKTIPSGLPKLY 312
DB 261 VAIEDEDLFGYPYLFRLGLSYNNKITEVQNGSLAVSNGNRELHLDNNLLSVPPGLSKLRS 320
QY 313 LQITLHNSIARVGVNDFCPTVPKMKKSLXSAISLFFNPNVYKWEQMPATFRCVLSRMSV 372
DB 321 LNVVYLHNSNKEIVKPTDFCPTVPKRAQYAGISLYDNPVKYWEVPPSVFRCVHHNNAI 380
QY 373 QLGN 376
DB 381 HFGS 384

RESULT 8
Q9DE01 PRELIMINARY; PRT; 224 AA.
AC Q9DE01;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Decorin (Fragment).
GN DCN.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'huigin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";
RL J. Mol. Evol. 51:363-373(2000).
DR EMBL: AF247824; AAG40159.1; -.
ZFIN: ZDB-GENE-010102-1; dcn.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00560; LRR; 7.
DR PRINTS: PR00019; LEURICHRPT.
DR SMART: SM00370; LRR; 5.
DR SMART: SM00369; LRR_Typ; 7.
FT NON_TER 1
FT NON_TER 224
FT NON_TER 224 AA; 24442 MW; 54A1B7AB91667DF0 CRC64;

Query Match 32.1%; Score 638.5; DB 13; Length 224;
Best Local Similarity 56.5%; Pred. No. 5.6e-38;
Matches 126; Conservative 37; Mismatches 59; Indels 1; Gaps 1;

QY 94 SVPTNIPFDTMLDLQNNKIKEIKENDFKGLTSLYGLILNENKLLKKTIPKAFUTTKLRR 153
DB 2 TVPEKIPLDTTLLDLQNNKITEIKENDFKGLTSLYGLILNENKLLKKTIPKAFUTTKLRR 61
QY 154 LYLHNSQLSEIPLNLPKSLABELRIHENKVKKIQKDTFGMNLHVLMSANPLDNNIGIEP 213
DB 62 LYLHNSQLSEIPLNLPKSLABELRIHENKVKKIQKDTFGMNLHVLMSANPLDNNIGIEP 121
QY 214 GAFEGV-TVFHIRIAEAKLTSPKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLG 272
DB 122 GAFADLKRVSARIADTNLTSPKGLPSSLPFELHDGDKITKVTADSLKGLNLSKLG 181
QY 273 NNLTKIHPKAPLTKKLRRLYLHNSQLSEIPLNLPKSLABELRIHENKVKKIQKDTFGM 315
DB 182 HNEISVWENGSLANVPHLRELHLENNALTAVPAGLADHKYIQV 224

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[illegible]

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC018370.1: -
DR InterPro: IPR003961: FN_III.
DR InterPro: IPR001611: LRR.
DR InterPro: IPR000483: LRR_Cterm.
DR InterPro: IPR000372: LRR_Nterm.
DR InterPro: IPR003592: LRR_out.
DR InterPro: IPR003591: LRR_Typ.
DR InterPro: IPR001211: PhospholipaseA2.
DR Pfam: PF00041: fn3; 1.
DR Pfam: PF00560: LRR; 7.
DR Pfam: PF01463: LRRCT; 1.
DR Pfam: PF01462: LRRNT; 1.
DR PRINTS: PR00019: LEURICHRPT.
DR SMART: SM00370: LRR; 3.
DR SMART: SM00082: LRRCT; 1.
DR SMART: SM00013: LRRNT; 1.
DR SMART: SM00369: LRR_Typ; 8.
DR PROSITE: PS00119: PA2_ASP; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 674 AA; 74087 MW; 38AB53F7243166CC CRC64;

Query Match 18.2%; Score 363.5; DB 4; Length 674;
Best Local Similarity 32.7%; Pred. No. 7.8e-18;
Matches 92; Conservative 51; Mismatches 105; Indels 33; Gaps 7;

QY 74 CPEGCYCSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 133

Db 54 CPEVCRDNGFYICNDRLTSIPDATTLYLQNNQI-----N 94

QY 134 NNLKTKIHPKAFLLTKRLRLYLSHNLSEIPLNPKSLAEIRHENKVKIKQDKTFKGM 193

Db 95 NAGI----PQDLKTKVNVQVITYLNDLDEFPINLPSRLHLQDNNVRTIARDSLARI 150

QY 194 NALHVLMSANPLDNNNGIEPGAF-EGVTVFHTRTAEAKLTSPKCLPPTLLEHLQYKI 252

Db 151 PULEKHLDDNSVTSVTEEDAFASKGLKLFJSRNHLSSIPGLPHTLEELRLDNNRI 210

QY 253 STVELEDFKRYKELQRLGLGNKKITD--IENGSLANIPRVREIHLNKKKKIPSGLP 310

Db 211 STIPLHAFKGLNSRLVLDGNLANQRIADDTFSRLQNLTELSLVRNSLAAPLNLP 269

QY 311 KYLQIFLHNSIARVGNDFCTVPKMKKSLYSALSIFNN 351

Db 270 AHLQKLYLDQNAISHIPYN---TLAKMRE--LERLDLSNN 304

RESULT 12

Q9DE02

ID Q9DE02 PRELIMINARY; PRT; 120 AA.

AC Q9DE02;

01-MAR-2001 (TREMBLrel. 16, Created)

01-MAR-2001 (TREMBLrel. 16, Last sequence update)

01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Biglycan-like protein 3 (Fragment).

GN BGL3 OR BGL3.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20496956; PubMed=11040287;

RA Shintani S., Sato A., Toyosawa S., O'huigin C., Klein J.;

RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.";

RL J. Mol. Evol. 51:363-373(2000).

DR EMBL: AF247823; AAC40158.1; -

DR ZFIN: ZDB-GENE-010131-5; bgl3.

DR InterPro: IPR001611; LRR.

DR InterPro: IPR003592; LRR_out.

DR InterPro: IPR003591; LRR_Typ.

DR Pfam: PF00560; LRR; 4.

DR SMART: SM00370; LRR; 3.
DR SMART: SM00369; LRR_Typ; 4.
FT NON_TER 1
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13569 MW; 37A302FB59F97696 CRC64;

Query Match 17.8%; Score 354; DB 13; Length 120;
Best Local Similarity 56.8%; Pred. No. 4.7e-18;
Matches 67; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 95 VPTNIPDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNKKLTKIHPKAFLLTKKLRRL 154

Db 2 VPKDIPANTLLDLQNNQITKEKDDFKGLDLNLYALFLLNNQISKIHPKAFRNMOKKLIL 61

QY 155 YLSHNLSEIPLNPKSLAEIRHENKVKIKQDKTFKGMNALHVLMSANPLDNNNGIE 212

Db 62 HLSYNLLTQMPENLPISVQSLRLHDNKKISRLPKGAFKGMHDLNVLSEANSPIANSID 119

RESULT 13

Q9WVC1

ID Q9WVC1 PRELIMINARY; PRT; 796 AA.

AC Q9WVC1;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE SLIT-2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE DAWLEY;

RX MEDLINE=99292758; PubMed=10364234;

RA Liang Y., Annan R.S., Carr S.A., Popp S., Mevissen M., Margolis R.K.;

RA Margolis R.O.;

RT "Mammalian homologues of the Drosophila slit protein are ligands of

the heparan sulfate proteoglycan glypican-1 in brain.";

RL J. Biol. Chem. 274:17885-17892(1999).

DR EMBL: AF141386; AAD38940.2; -

DR InterPro: IPR001611; LRR.

DR InterPro: IPR000483; LRR_Cterm.

DR InterPro: IPR000372; LRR_Nterm.

DR InterPro: IPR003592; LRR_out.

DR InterPro: IPR003591; LRR_Typ.

DR Pfam: PF00560; LRR; 13.

DR Pfam: PF01463; LRRCT; 3.

DR Pfam: PF01462; LRRNT; 4.

DR PRINTS: PR00019; LEURICHRPT.

DR SMART: SM00370; LRR; 7.

DR SMART: SM00082; LRRCT; 3.

DR SMART: SM00013; LRRNT; 4.

DR SMART: SM00369; LRR_Typ; 4.

SQ SEQUENCE 796 AA; 89542 MW; 0F50806FC0345005 CRC64;

Query Match 17.1%; Score 340.5; DB 11; Length 796;

Best Local Similarity 26.1%; Pred. No. 4.1e-16;

Matches 111; Conservative 55; Mismatches 120; Indels 139; Gaps 13;

QY 74 CPEGCYCSRVVHCSDLGLTSVPTNIPDTRMLDLQNNKIKEIKENDFKGLTSLYGLILN 108

Db 277 CPIACTSSNNIVDCRGKGLTEIPTNLP-EFITEIRLEQNSIRVIPPCCATSPYKKLRDL 335

QY 109 QNNKIKEIKENDFKGLTSLYGLILNKKLTKIHPKAFLLTKKLRRLYLSHNLSEIPLNL 168

Db 336 SNNQISELAPDAFQGLRSLNSLVLYGNKKTLPKSLFEGFLSQLLLNANKINCLRVDA 395

QY 169 PKSLAEIR---IHENKVKIKQDKTFKGMNALHVLMSANP-----LDNNGIE 212

Db 396 FQDLHNLNLLSYDNKIQIVAKGTFESALRAIQTMHLAQNPFTCDCHLKWLYADLYLHTNPI 455

QY 213 -PGA-----FEQVTVFH 223

Db 456 TSGARCTSPRLANKRIGQIKKKFKRCGTEGYRSKLSGDCFADLACPEKRCCEGTV-- 513
QY 224 IRIAEAKLTSPKGLPTLLELHDYNKISTVELED-FKRYKELQRLGLGNKKTIDENG 282
Db 514 -DCSNQKLNKIPHIPOYTAEELRLNNEFTVLEATGIEFKLPQRLKINLSNKKITDIEG 572
QY 283 SLANIPRVREIHLNKKL----KIPSGPELKYQITIFLHNSIARVGVNDPCPTVPK 338
Db 573 AFEAGSGVNEILLTSNRLNENVQHKMFGLSLATL---MLRSNRISCVGNDSEFTGLGSVR 629
QY 339 KKSLEY-----SATSFLNPNVYKWMOPATERC-----VLSRMS 371
Db 630 LLSLYDNOITTVAPGAFGLTSLSLTLNLANP-----PNCNCHLAWLGEWLRKR 679
QY 372 VOLGN 376
680 IVTGN 684

Query Match 16.9%; Score 336; DB 4; Length 1525;
Best Local Similarity 26.5%; Pred. No. 1.9e-15;
Matches 105; Conservative 61; Mismatches 120; Indels 110; Gaps 12;

QY 74 CPFGCQCYSRVHVCSDGLTSTVPTNIPEDT-----RMLDL 108
Db 277 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVIPPGAESPYYKLRIDL 335
QY 109 QNNKIKEIKENDFKGLTSLYGLILNKNKLTIKHPKAFITTKLRRLYLHNSQLSEIPLNL 168
Db 336 SNNQISELAPDAFOGLRSLNSLVYGNKITELPKSLFEGFLSLQLLLNANKINCLRVDA 395
QY 169 PKSLAELR---IHENKVKIKQDKTFKGMNALHVLMSANP-----LNNNGIE 212
Db 396 FOOLHNLNLLSLYDNKIQITIAKGTFSPLRAIQTMHLAQNPFICDCHLKWLDLHTNPTE 455
QY 213 -PCA-----FEQVTVFH 223
Db 456 TSGARCTSPRLANKRIGQIKKKFKRCGTEGYRSKLSGDCFADLACPEKRCCEGTV-- 513
QY 224 IRIAEAKLTSPKGLPTLLELHDYNKISTVELED-FKRYKELQRLGLGNKKTIDENG 282
Db 514 -DCSNQKLNKIPHIPOYTAEELRLNNEFTVLEATGIEFKLPQRLKINLSNKKITDIEG 572
QY 283 SLANIPRVREIHLNKKL----KIPSGPELKYQITIFLHNSIARVGVNDPCPTVPK 338
Db 573 AFEAGSGVNEILLTSNRLNENVQHKMFGLSLATL---MLRSNRITCVGNDSEFTGLGSVR 629
QY 339 KKSLEY-----SATSFLNPNVYKWMOPATERC-----VLSRMS 371
Db 630 LLSLYDNOITTVAPGAFGLTSLSLTLNLANP-----PNCNCHLAWLGEWLRKR 679
QY 372 VOLGN 376
680 IVTGN 684

RESULT 14
QY507 PRELIMINARY; PRT; 1525 AA.
AC QY507;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE SLIT2.
GN SLIT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=99200389; PubMed=10102268;
RA Brose K., Bland K.S., Wang K.H., Arnott D., Henzel W., Goodman C.S.,
RA Tessier-Lavigne M., Kidd T.;
RT "Slit proteins bind Robo receptors and have an evolutionarily
RT conserved role in repulsive axon guidance."
RL Cell 96:795-806(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=99200391; PubMed=10102268;
RA Brose K., Bland K.S., Wang K.H., Arnott D., Henzel W., Goodman C.S.,
RA Tessier-Lavigne M., Kidd T.;
RT "Slit proteins bind Robo receptors and have an evolutionarily
RT conserved role in repulsive axon guidance."
RL Cell 96:795-806(1999).
RN [2]

DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FOLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 6.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR KQ Calcium-binding; EGF-like domain; Glycopolprotein; Repeat.
SW SEQUENCE 1525 AA; 169394 MW; 8A8ICDE34EF06A73 CRC64;
Query Match 16.9%; Score 336; DB 4; Length 1525;
Best Local Similarity 26.5%; Pred. No. 1.9e-15;
Matches 105; Conservative 61; Mismatches 120; Indels 110; Gaps 12;

QY 74 CPFGCQCYSRVHVCSDGLTSTVPTNIPEDT-----RMLDL 108
Db 277 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVIPPGAESPYYKLRIDL 335
QY 109 QNNKIKEIKENDFKGLTSLYGLILNKNKLTIKHPKAFITTKLRRLYLHNSQLSEIPLNL 168
Db 336 SNNQISELAPDAFOGLRSLNSLVYGNKITELPKSLFEGFLSLQLLLNANKINCLRVDA 395
QY 169 PKSLAELR---IHENKVKIKQDKTFKGMNALHVLMSANP-----LNNNGIE 212
Db 396 FOOLHNLNLLSLYDNKIQITIAKGTFSPLRAIQTMHLAQNPFICDCHLKWLDLHTNPTE 455
QY 213 -PCA-----FEQVTVFH 223
Db 456 TSGARCTSPRLANKRIGQIKKKFKRCGTEGYRSKLSGDCFADLACPEKRCCEGTV-- 513
QY 224 IRIAEAKLTSPKGLPTLLELHDYNKISTVELED-FKRYKELQRLGLGNKKTIDENG 282
Db 514 -DCSNQKLNKIPHIPOYTAEELRLNNEFTVLEATGIEFKLPQRLKINLSNKKITDIEG 572
QY 283 SLANIPRVREIHLNKKL----KIPSGPELKYQITIFLHNSIARVGVNDPCPTVPK 338
Db 573 AFEAGSGVNEILLTSNRLNENVQHKMFGLSLATL---MLRSNRITCVGNDSEFTGLGSVR 629
QY 339 KKSLEY-----SATSFLNPNVYKWMOPATERC-----VLSRMS 371
Db 624 GLSSVLLSLYDNOIT--TVAPGAFDTLSLSTLNL 657
RESULT 15
QY507 PRELIMINARY; PRT; 1529 AA.
AC QY507;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE SLIT-2 protein.
GN SLIT-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99033071; PubMed=9813312;
RA Itoh A., Miyabayashi T., Ohno M., Sakano S.;
RT "Cloning and expressions of three mammalian homologues of drosophila
RT slit suggest possible roles for slit in the formation and maintenance
RT of the nervous system."
RL Brain Res. Mol. Brain Res. 62:175-186(1998).
DR EMBL; AB017168; BAA35185.1; -.
DR HSSP; P00743; ICCF.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.

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DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR003645; FcIn.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF_9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00001; EGF_like; 7.
DR SMART; SM00274; FcIn; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00370; LRR; 6.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW Calcium-binding; EGF-like domain; Glycoprotein; Repeat.
SQ { SEQUENCE 1529 AA; 169869 MW; 5D19CG5E7FD461BA CRC64;

Query Match          16.9%; Score 336; DB 4; Length 1529;
Best Local Similarity 26.0%; Pred. No. 1.9e-15;
Matches 105; Conservative 61; Mismatches 120; Indels 118; Gaps 12;

QY 74 CPFGQCYSRVVHCSDGLTSVPTNIPDTPD-----RMLDL 108
DB 273 CPAACTCSNNIVDCRGKGLTEIPTNLP-ETITEIRLEQNTIKVPPGAFSPYKKLRIDL 331

QY 109 ONNKIKETKENDEKGLTSLYLNNKLTIKHPKALTTKKLRRLYLSHNOLSEIPLNL 168
DB 332 SNNQISELAPDAGFGLRSLNLYGNKTELPSLEGLFSQLQLLLNANKINCLRVDA 391

QY 169 PKSLAELR---IHENKVKIKQDTFGMNAHLVLEMSANP-----LDNNGIE 212
DB 392 FQDLHNLNLSLYDNKLOTIAKTFSPLRALQTMHLAQNPFICDCHLKLADYLHTNP 451

QY 213 -----PGA----- 215
DB 452 TSGARCTSPRLANKRIGQIKSKKFCRSKQYFIPGTEYRSLSGDCFADLACPEKCR 511

QY 216 FEGTVFHIRIAEAKLTSPKGLPPTLLEHLHDYKNKISTVELED-FKRYKELQRLGLGNN 274
DB 512 CEGTIV---DCSNOKLNKIPHIPOYTAEURLNNEFTVLEATGIFKKLPOLRKINFNN 568

QY 275 KITDIENGLANIPRVRIHLENKCLK-----KIPSGLPKELKYLQIIEFHSNSTARVGND 330
DB 569 KITDIEGAFEGASGVNEILLTSNRLENVQHMKFGLESCLKL---MLRSNRITCVGND 625

QY 331 FCPVTPKMKSLYSALSNPNVYWEQPATFRCVLRSMSVOL 374
DB 626 F-----IGLSSVRLSLYDNOIT--TVAPGAFDTLHSLSLTNL 661
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Search completed: May 27, 2003, 16:05:11
Job time : 39 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 16:01:11 ; Search time 22 seconds
(without alignments)
1656.134 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFFS.....PATERCVLSRMSVQLNGFM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1040.5	52.2	369	2 S32793	biglycan precursor
2	1037.5	52.1	369	2 S20811	proteoglycan I - m
3	1034	51.9	368	1 BGHUN	biglycan precursor
4	1024.5	51.4	369	2 S32559	biglycan precursor
5	969	48.6	357	2 S24317	decorin precursor
6	963.5	48.4	359	1 NBHUC8	decorin precursor
7	943	47.3	360	2 S06280	decorin precursor
8	941	47.2	360	2 I47020	decorin - rabbit
9	907.5	45.6	354	2 A5454	decorin precursor
10	899	45.1	354	2 S29145	decorin precursor
11	399.5	20.1	343	2 A41748	lumican precursor
12	384	19.3	342	2 A46743	lumican precursor
13	378	19.0	338	2 S52284	lumicon, secretory
14	358.5	18.0	382	2 I39088	proline- arginine-
15	342.5	17.2	375	2 S05390	fibromodulin precu
16	333.5	16.7	380	2 S71876	fibromodulin - chi
17	324	16.3	1523	2 T13953	MEGF5 protein - ra
18	323	16.2	1531	2 T42218	slit-1 protein hom
19	318	16.0	376	2 S52275	fibromodulin precu
20	316	15.9	1469	2 B36665	slit protein 2 pre
21	316	15.9	1480	2 A36665	slit protein 1 pre
22	296	14.9	1091	2 A58532	glial cell membran
23	294	14.8	361	2 A53860	chondroadherin pre
24	282.5	14.2	1025	2 T42626	secreted leucine-r
25	272	13.7	603	2 JC1282	insulin-like growt
26	266	13.4	707	2 JC7763	neuronal leucine-r
27	265	13.3	603	2 JC6128	insulin-like growt
28	265	13.3	1051	2 T13174	gp150 protein - fr
29	261.5	13.1	907	2 JG0193	G protein-coupled

30	260.5	13.1	680	2 T19939	hypothetical prote
31	260.5	13.1	738	2 T19938	hypothetical prote
32	251.5	12.6	907	2 JE0176	orphan G protein-c
33	249	12.5	322	2 S72271	proteoglycan Lb pr
34	246	12.3	605	2 A41915	insulin-like growt
35	245	12.3	662	2 S42799	garp precursor - h
36	241	12.1	605	2 JC5239	insulin-like growt
37	235.5	11.8	298	2 JC4130	osteoglycin precu
38	234	11.7	333	2 T34555	hypothetical prote
39	230	11.5	536	2 A34901	lysine carboxypept
40	225.5	11.3	1389	2 T13852	gene wheeler prote
41	223.5	11.2	1385	2 T13887	tlr protein - frui
42	223	11.2	559	2 T42998	Ras-binding protei
43	223	11.2	594	2 T23841	hypothetical prote
44	223	11.2	610	2 T23836	hypothetical prote
45	219	11.0	572	2 T30947	hypothetical prote

ALIGNMENTS

RESULT 1
S32793

biglycan precursor - rat

N:Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteoglycan I core prot
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-Aug-1999
C:Accession: S32793

R:Dröher, K.L.; Asundi, V.; Matzura, D.; Cowan, K.

Eur. J. Cell Biol. 53, 296-304, 1990

A:Title: Vascular smooth muscle biglycan represents a highly conserved proteoglycan w

A:Reference number: S32793; MUID:91184222; PMID:2081545

A:Accession: S32793

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-369 <DRE>

A:Cross-references: GB:U17834; NID:g600497; PIDN:AAA58797.1; PID:g600498

C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc

F:1-16/Domain: chondroitin sulfate proteoglycan; dermatan sulfate; extracellular matrix;

F:17-37/Domain: signal sequence #status predicted <PRO>

F:38-369/Product: biglycan #status predicted <PRO>

F:58-82/Domain: proteoglycan amino-terminal homology <PAH>

F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F:185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F:255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F:279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F:302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical

F:317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>

F:42,48,181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted

F:271,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.2%; Score 1040.5; DB 2; Length 369;

Best Local Similarity 52.8%; Pred. No. 1.2e-63;

Matches 199; Conservative 67; Mismatches 93; Indels 19; Gaps 3;

Qy 4 YVLLFLALCSAKPFF----FSPSHIALKNMMLKMDTDDDDDDDDDDDDNSLFPPT 59

Db 5 WLLTLLALSOALPFEKGFWDFTLDDGLLMMNDEASGSDTTSGVPDL- ---SLTPT- 59

Qy 60 EPRSHPFFDLFPMCPGCCYRVVHCSDLGTSVPTNTPTFTRMLDQNNKIKEKEN 119

Db 60 -----FSAMCPGCHCLRVVQCSDLGKTVPKETSPDTLLDQNNISELRKD 109

Qy 120 DFKGLTSLYLILNKKLTTHPKAFITTKLRRLYSHNQLSEIPLNLPKSLAEIRHE 179

Db 110 DFKGLQHLVALVLNKKISKIHEKAFSPDRKLOKLYISKNNHLVEIPNLPSSSLVELRIHD 169

R:Roughley, P.J.; White, R.J.
 Biochem. J. 262, 823-827, 1989
 A:Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties of
 A:Reference number: S05639; MUID:90073579; PMID:2590169
 A:Accession: S05639
 A:Molecule type: protein
 A:Residues: 38-41, 'X', 43-46, 'X', 48-57 <ROU>
 R:Fisher, L.W.; Hawkins, G.R.; Tuross, N.; Termino, J.D.
 J. Biol. Chem. 262, 9703-9708, 1987
 A:Title: Purification and partial characterization of small proteoglycans I and II, bone
 A:Reference number: A92656; MUID:87250639; PMID:3597437
 A:Accession: A28457
 A:Molecule type: protein
 A:Residues: 38-41, 'X', 43-62, 'X', 64-66 <FIS3>
 A:Experimental source: bone
 C:Genetics:
 A:Gene: GDB:BGN
 A:Cross-references: GDB:119727; OMIM:301870
 Map position: Xq28-Xq28
 A:Introns: 80/1; 117/3; 189/1; 226/1; 257/2; 303/3
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
 C:Keywords: chondroitin sulfate proteoglycan; dermatan sulfate; duplication; extracellular
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-37/Domain: propeptide #status predicted <PRO>
 F:38-368/Product: biglycan #status predicted <MAT>
 F:57-81/Domain: proteoglycan amino-terminal homology <PAH>
 F:91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:115-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:139-159/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:160-183/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:184-207/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:209-229/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:230-253/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:254-277/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:278-300/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:301-315/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F:316-368/Domain: proteoglycan carboxyl-terminal homology <PCH>
 F:42,47/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
 F:180,198/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
 F:270,311/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 1034; DB 1; Length 368;
 Best Local Similarity 53.2%; Pred. No. 3 4e-63;
 Matches 200; Conservative 63; Mismatches 93; Indels 20; Gaps 3;

6 LLLFLALCSAKFP-----FSPSHLAKNMMLKDMEDTDDDDDDDDDDDDSDNSLFTREP 61
 7 LVSLALQSALPFEQGRGDFDTLDDGPFWMNDREASGADTSGVLDPD-----SVIPTY- 60
 QY 62 RSHFFPDLFPMCPFCGCYSRVHVCHSDGLTSVPTNIFDTRMLDLQNNKKEIKENDF 121
 Db 61 -----AMCPFGCHLRVVOCSDLGLSVKPEISPDPTTLLDLQNNDISLRKDDF 110
 QY 122 KGTSYGLILNNKUTKIHPRAFITTKRLRLYLSHNOLSEIPLNPKSLAELRTHENK 181
 Db 111 KGLQHYALVLYNNKISKIHERAFSLRKLQKLYTSKNHILVEIPNPLPSVLRLHNR 170
 QY 182 VKIQDPTFGMMALHVLMSANPLDNNIGEPAGFVGTVFHIRIAEAKLTSVPKGLPPT 241
 Db 171 IRKVPKGVSGFLNMMCIEMGNPLNSGFEPCGAFDGLKLVLRISAKLTGPKDLPET 230
 QY 242 LLEHLYNNKISVLEDEKRYKELQRLGLGNKTKITDIENGLANTPVRETHLENNK 301
 Db 231 LNELHLDHNNKIQAELEDLRLYSKLYRGLGHNGHQRMIENGSLSPFTLRLEHLDNNK 290
 QY 302 KIPSGLPKLYLQITFLHNSIARVGVNDPCFVPMKSKLSAISLFPNNPVKYMOWEOPA 361
 Db 291 RVPSGLPDLKLLQVYLYHNSNITKVGNDPCFPGVCRKAYNGISLFPNNPVYVEVOPA 350
 QY 362 TFCVLSRMSVQLGNF 377
 Db 351 TFCVTDRLAIQFGNY 366

RESULT 4

S32559
 biglycan precursor - bovine
 N:Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteochondroitin core p
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C:Accession: S32559; S34229; A33701; A31430; PT0078; S55673; A33137
 R:Torok, M.A.; Evans, S.A.S.; Marcum, J.A.
 Biochim. Biophys. Acta 1173, 81-84, 1993
 A:Title: cDNA sequence for bovine biglycan (PGI) protein core.
 A:Reference number: S32559; MUID:93250052; PMID:8485158
 A:Accession: S32559
 A:Molecule type: mRNA
 A:Residues: 1-369 <TOR>
 A:Cross-references: EMBL:L07953; NID:gl62746
 A:Experimental source: aortic smooth muscle
 R:Marcum, J.A.; Torok, M.; Evans, S.
 Submitted to the EMBL Data Library, December 1992
 A:Reference number: S34229
 A:Accession: S34229
 A:Molecule type: mRNA
 A:Residues: 1-250, 'V', 252-369 <MAR>
 A:Cross-references: EMBL:L07953
 R:Neame, P.J.; Choi, H.U.; Rosenberg, L.C.
 J. Biol. Chem. 264, 8653-8661, 1989
 A:Title: The primary structure of the core protein of the small, leucine-rich proteog
 A:Reference number: A33701; MUID:89255324; PMID:2656687
 A:Accession: A33701
 A:Molecule type: protein
 A:Residues: 38-187, 'E', 189-367, 'Y' <NEA>
 A:Experimental source: cartilage
 R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.
 J. Biol. Chem. 264, 2876-2884, 1989
 A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII,
 A:Reference number: A31430; MUID:89123388; PMID:2914936
 A:Accession: A31430
 A:Molecule type: protein
 A:Residues: 38-41, 'X', 43-47, 'X', 49-63 <CHO>
 A:Note: sequences from skin and cartilage were identical
 R:Marcum, J.A.; Thompson, M.A.
 Biochem. Biophys. Res. Commun. 175, 706-712, 1991
 A:Title: The amino-terminal region of a proteochondroitin core protein, secreted by a
 com human bone.
 A:Reference number: PT0077; MUID:91207372; PMID:2018513
 A:Accession: PT0078
 A:Molecule type: protein
 A:Residues: 17-24, 'F', 26-30 <MA2>
 A:Experimental source: aortic smooth muscle
 R:Scott, P.G.; Nakano, T.; Dodd, C.M.
 Biochim. Biophys. Acta 1244, 121-128, 1995
 A:Title: Small proteoglycans from different regions of the fibrocartilaginous tempo
 A:Reference number: S55673; MUID:95284073; PMID:7766647
 A:Accession: S55673
 A:Molecule type: protein
 A:Residues: 38-41, 'X', 43-47, 'X', 49-53 <SCO>
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc
 C:Keywords: cartilage; chondroitin sulfate proteoglycan; dermatan sulfate; extracellu
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-37/Domain: amino-terminal propeptide #status predicted <PRO>
 F:38-369/Product: biglycan #status predicted <MAT>
 F:92-115/Domain: proteoglycan amino-terminal homology <PAH>
 F:116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:317-369/Domain: proteoglycan carboxyl-terminal homology <PCH>

C:Accession: S06280; B31430; A26545; A20935
 Bay, A.; McQuillan, C.I.; Termino, J.D.; Young, M.R.
 Biochem. J. 248, 801-805, 1987
 A:Title: Molecular cloning and sequence analysis of
 the cDNA for small proteoglycan I
 A:Reference number: S06280; MUID:88133946; PMID:3435485
 A:Accession: S06280
 A:Molecule type: mRNA

A:Residues: 1-360 <DAY>
A:Cross-references: EMBL:Y00712; NID:g618; PIDN:CAA68702.1; PID:g619
A:Experimental source: bone
R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.
J. Biol. Chem. 264, 2876-2884, 1989
A:Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII,
A:Reference number: A31430; MUID:89123388; PMID:2914936
A:Accession: B31430
A:Molecule type: protein
A:Residues: 31-33, X', 35-54 <CHO>
A:Experimental source: cartilage; fetal skin
R:Coster, L.; Rosenberg, L.C.; van der Rest, M.; Poole, A.R.
J. Biol. Chem. 262, 3809-3812, 1987
A:Title: The dermatan sulfate proteoglycans of bovine sclera and their relationship t
A:Reference number: A26545; MUID:87137687; PMID:3818667
A:Accession: A26545
A:Molecule type: protein
A:Residues: 31-50 <COS>
A:Experimental source: sclera
R:Pearson, C.H.; Winterbottom, N.; Fackre, D.S.; Scott, P.G.; Carpenter, M.R.
J. Biol. Chem. 258, 15101-15104, 1983
A:Reference number: A20935; MUID:84087911; PMID:6654908
A:Accession: A20935
A:Molecule type: protein
A:Residues: 31-54 <PEA>
A:Experimental source: skin

R.; Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Fackre, D.S.; Scott, P.G. *Biochem. J.* 232, 277-279, 1985

nces around glycosylation sites in different proteoglycans.
 A:Reference number: A44700; MUID:86103195; PMID:3936484
 A:Contents: annotation; glycosylation
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc
 C:Keywords: chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; ext
 F:1-15/Domain: signal sequence #status predicted <Sig>
 F:16-30/Domain: propeptide #status predicted <PRO>
 F:31-36/Product: decorin #status predicted <MAT>
 F:49-73/Domain: proteoglycan amino-terminal homology <PAH>
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F:309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>
 F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
 F:190_326/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
 F:212_263_304/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.3%; Score 943; DB 2; Length 360;
 Best Local Similarity 49.1%; Pred. No. 5,3e-57;
 Matches 186; Conservative 69; Mismatches 102; Indels 22; Gaps 5;

[illegible]

101 DFNKLNKLTLLINNKISKSPGAFAPLVKLERLYLSKNQKELPEKMPKTLOELRVHE 160
180 NKVKIKQKDTFGKMAHVLHLENSANPLDNNIEGPAFEGV-TVFHRTAEAKLTSPKGL 238
161 NEITKVRKSVFNGLNQMTIVELGTNPLKSSGTENGAFQGMKKLSYIRIADTNITIPQGL 220
239 PPTLEHLHDYNKISTVELEDFKRYKELQRLGLGNKKTIDTENGSLANIIPRVREIHLENN 298
221 PPSLTLEHLHDGNGKITKVDAAISLGLNNLAKLGLSFSISAVDNGSLANTPHLEHLN 280
299 KKKIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSLENPNVKYWM 358
281 KLAKEPGGVADHKYIQVYVLLHNNISAGNSDFCPCPGYNTKKASYSGVSLFNPVQYWEI 340
359 QPATFRCVLSRMSVOLGNF 377
341 QPSTFRVCYVRAAVQLGNY 359

RESULT 8

147020

Species: *Oryctolagus cuniculus* (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
C:Accession: I47020
R:Zhan, Q.; Burrows, R.; Cintron, C.
Invest. Ophthalmol. Vis. Sci. 36, 206-215, 1995
A:Title: Cloning and in situ hybridization of rabbit decorin in corneal tissues.
A:Reference number: I47020; MUID:95122319; PMID:7822148
A:Accession: I47020
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-360 <ZHA>

A:Cross-references: GB:S76584; NID:g913374; PIDN:AB33083.1; PID:g913375
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
F:49-73/Domain: proteoglycan amino-terminal homology <PAH>
F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:131-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 47.2%; Score 941; DB 2; Length 360;

Best Local Similarity 49.6%; Pred. No. 7.3e-57;

Matches 188; Conservative 67; Mismatches 102; Indels 22; Gaps 5;

QY 1 MKEYVLLFLALCS-AKPFSPSHIALKNMKLKMEDTDDDDDDDDDDDDSLFPT 59
DB 1 MTATLILLIAQVSWAGPP---QORGLDFPMLD-EASIGDFEAPLPDLM----- 50

QY 60 EPRSFFFDLPFMPGCGQCYSRVHVHSDGLTSVPTNIPDTRMLDQNNKIKEIKEN 119
DB 51 -----LGPVCPFCQCHLRVVOCSDLGLDKVPKDPDPTLLDQNNKITEIKDG 100

QY 120 DFKGLTSLYGLLNNKLTIKHPKAFLTITKLRRLYLSHNLSEIPLNPKSLAEIRTHE 179
DB 101 DFNKLNKHALILVNNKISKISPGAFPLVLERLYLSKNHLEKPEKMPKSLQELRAHE 160

QY 180 NKVKTKOKDTFGKMAHVLHLENSANPLDNNIEGPAFEGV-TVFHRTAEAKLTSPKGL 238
DB 161 NEITKVRKSVFSGMOMIVELGTNPLKSSGTENGAFQGMKKLSYIRIADTNITIPQGL 220

QY 239 PPTLEHLHDYNKISTVELEDFKRYKELQRLGLGNKKTIDTENGSLANIIPRVREIHLENN 298
DB 221 PPSLTLEHLHDGNGKITKVDAAISLGLNNLAKLGLSFSISAVDNGSLANAPHLEHLN 280

QY 299 KKKIPSGLPKLYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSLENPNVKYWM 358
DB 281 KLIRVPEGLADHKYIQVYVLLHNNISVWGANDFCPPGYNTKKASYSGVSLFNPVQYWEI 340
QY 359 QPATFRCVLSRMSVOLGNF 377
DB 341 QPSTFRVCYVRAAVQLGNY 359

RESULT 9

A55454

decorin precursor - mouse
N:Alternate names: proteoglycan II
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 20-Aug-1999
C:Accession: A55454; S20812
R:Scholzen, T.; Solursh, M.; Suzuki, S.; Reiter, R.; Morgan, J.L.; Buchberg, A.M.; Si
J. Biol. Chem. 269, 28270-28281, 1994
A:Title: The murine decorin. Complete cDNA cloning, genomic organization, chromosomal
A:Reference number: A55454; MUID:95050610; PMID:7961765
A:Accession: A55454
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-354 <SCH>
A:Cross-references: GB:X53929; NID:g53668; PIDN:CAA37876.1; PID:g53669
R:Naotoh, Y.; Suzuki, S.
Submitted to the EMBL Data Library, July 1990
A:Description: Nucleotide sequences of cDNAs encoding mouse PGI and PGII.
A:Reference number: S20811
A:Accession: S20812
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-354 <NAI>

A:Cross-references: EMBL:X53929; NID:g53668; PIDN:CAA37876.1; PID:g53669
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc
C:Keywords: collagen binding; extracellular matrix; glycoprotein
F:1-16/Domain: signal sequence #status predicted <PRO>
F:17-30/Domain: proteoglycan amino-terminal homology <PAH>
F:43-67/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:125-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:196-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:288-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 45.6%; Score 907.5; DB 2; Length 354;

Best Local Similarity 52.0%; Pred. No. 1.4e-54;

Matches 170; Conservative 65; Mismatches 87; Indels 5; Gaps 2;

QY 56 FTREPSRSHFFPD---LFPMPGCGQCYSRVHVHSDGLTSVPTNIPDTRMLDQNN 111
DB 27 FMLEDEASGIIPDDPNLISMCPYRCQCHLRVVOCSDLGLDKVPDFPDPTLLDQNN 86

QY 112 KIKETKENDKGLTSLYGLLNNKLTIKHPKAFLTITKLRRLYLSHNLSEIPLNPKS 171
DB 87 KITEKEGAFKNDLHTLLVNNKISKISPEAKPLVLERLYLSKNQKELPEKMPRT 146

QY 172 LAELRIENKVKTKOKDTFGKMAHVLHLENSANPLDNNIEGPAFEGV-TVFHRTAEAK 230
DB 147 LQELRVHENEITKLRKSDFNGLNNVLELGNPLKSSGTENGAFQGLKSLYSIRISDTN 206

QY 231 LTSVPKGLPPTLLEHLHDYNKISTVELEDFKRYKELQRLGLGNKKTIDTENGSLANIIPRV 290
DB 207 ITAIPQGLTSLTEVHLDGNGKITKVDAPLSKGLNLSKLSFNSITVMENGLANVPHL 266

QY 291 REITHLENNKLTSPGPELKYLOIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSLEN 350
DB 221 PPSLTLEHLHDGNGKITKVDAAISLGLNNLAKLGLSFSISAVDNGSLANAPHLEHLN 280

Db 267 RELHLDNKKLLRPAGLAQHKKYIQVYVLLHNNNTISAVQNDFCRAGHPSPRKASYSAVSLYG 326

Oy 351 NPVKYEWQPATPCFVLRSMSVOLGNF 377
|||||:|||||:|||||:|||||:

Db 327 NPVRYWEIFNTFCVYVRSALQIGNY 353

RESULT 10

S29145
decorin precursor - rat
N:Alternate names: dermatan sulfate proteoglycan-II
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S29145; 160238; S28517
R:Abramson, S.K.; Woessner Jr., J.F.
Biochim. Biophys. Acta 1132, 225-227, 1992
A:Title: cDNA sequence for rat dermatan sulfate proteoglycan-II (decorin).
A:Reference number: S29145; MUID:93003331; PMID:1390895
A:Accession: S29145
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-354 <ABR>
A:Cross-references: EMBL:212298; NID:g57549; PIDN:CAA78170.1; PID:g57550
R:Asundi, V.K.; Dreher, K.L.
Eur. J. Cell Biol. 59, 314-321, 1992
A:Title: Molecular characterization of vascular smooth muscle decorin: deduced core prot
A:Reference number: 160238; MUID:93154359; PMID:1493796
A:Accession: 160238
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 11-354 <RES>
A:Cross-references: EMBL:X59859; NID:g56056; PIDN:CAA42519.1; PID:g56057
C:Genetics:
A:Gene: DCN
C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology: proteoglycan
C:Keywords: collagen binding; extracellular matrix; glycoprotein
F:1-30/Domain: signal sequence (fragment) #status predicted <SIG>
F:31-354/Product: decorin #status predicted <MAT>
F:43-67/Domain: proteoglycan amino-terminal homology <PAH>
F:77-100/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:125-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:170-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:196-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:217-240/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:241-264/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:265-287/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:288-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:303-354/Domain: proteoglycan carboxyl-terminal homology <PCH>
F:303-354/Domain: proteoglycan carboxyl-terminal homology #status atypical <LRR>

Query Match	45.1%	Score	899;	DB 2;	Length	354;			
Best Local Similarity	46.5%;	Pred. No.	5.2e-54;						
Matches	178;	Conservative	70;	Mismatches	99;	Indels	36;	Gaps	5;
QY	1	MKEYVLLFLALCS-AKPFPSHTALKNNMLKMDMEDTDDDDDDDDDDDDDDDDDDNSLPFTR	59						
Db	1	MKATLVFLLAQVSWAGPF---EQRGLDFMLED-----	31						
QY	60	EPRSFFPFD---LFPMGPFQCQSYRVVHGSDLGLTSVPTNIPEDTRMLDLONNKIKE	115						
Db	32	-EASGIIPYDPDNPLISMCPYRCQCHLRVVQCSGLGDKVPWEFPEDTLLDLONNKITE	90						
QY	116	IKENDPKGLTSLYGLLNNKLTTHPKAFLTKKRLRLYLSHNQSLSEIPLNPKSLAEL	175						
Db	91	IREGAFNKUDLHTLLVNNKTSLSPEAFPLVKLERLYLSKNHUKELPEKLPKTLQEL	150						
QY	176	RIHENVKVKIQRDTFKGMNALHVLSEANSPLDNNGIEPCAFEGVT-VFHIRIAEAKLTSV	234						
Db	151	RLHDNEITLKKSVFNGLRMLVIELGGNPKNLSGIENGALOGMKGLYIRISDTNITAI	210						
QY	235	PKGLPPTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANIPRVRETH	294						

Db	211	PQGLPTSGISELHLDGNKIAKVDAASLKMNSLKLGSFNSITVVGNSLANVPHLRELH	270
QY	295	LENNKLLKIFSGPELKYLOIIFUHSNSIARGVYNDFCPTVPMKKKSLYSALSFNPNPVK	354
Db	271	LNNKLLRVFAGLAQHKYQVVYLHNNISVGGHDFCLPSYQTRKTSYAVLSYSPVR	330
QY	355	YWEMQPATRCFVLSRMSVQLGNF	377
Db	331	YWQIHPTFCVFCGRSTIQLGNY	353

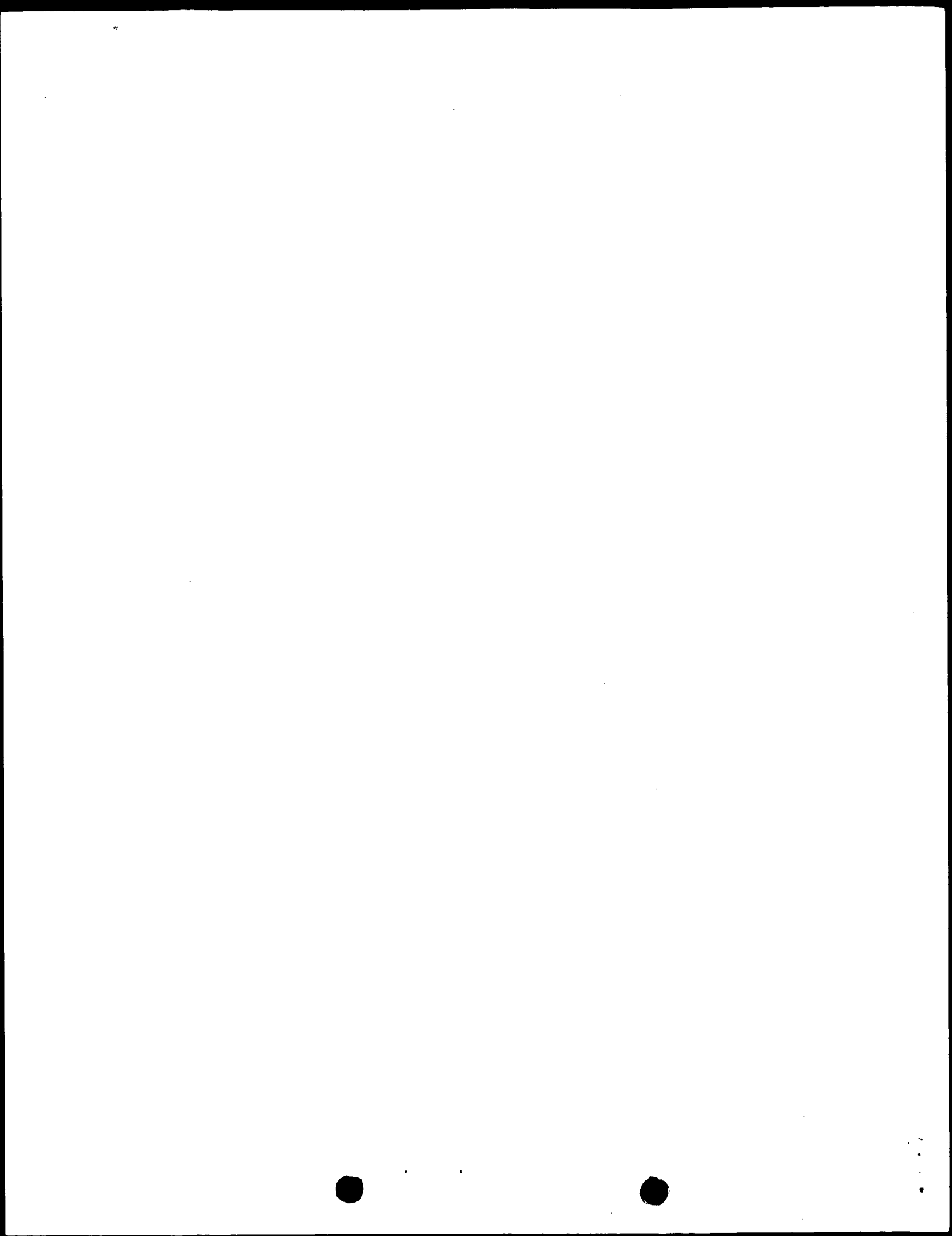
RESULT 11
A41748
luminan precursor - chicken
N:Alternate names: corneal keratan sulfate proteoglycan
C:Species: Gallus gallus (chicken)
C:date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 04-Sep-1998
C:Accession: A41748; B41748
R:Blöcherberger, T.C.; Vergnes, J.P.; Hempel, J.; Hassell, J.R.
J. Biol. Chem. 267, 347-352, 1992
A:title: cDNA to chick luminan (corneal keratan sulfate proteoglycan) reveals homolog
A:Reference number: A41748; MUID:92112674; PMID:1370446
A:Accession: A41748
A:Molecule type: mRNA
A:Residues: 1-343 <BL1>
A:Cross-references: GB:M80584
A:Accession: B41748
A:Molecule type: protein
A:Residues: 55-76 <BL2>
C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C:Keywords: glycoprotein; tandem repeat
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-343/Product: luminan #status predicted <MAT>

Query Match 20.1%; Score 399.5; DB 2; Length 343;
Best Local Similarity 31.98; Pred. No. 5.5e-20;
Matches 104; Conservative 72; Mismatches 125;
Indels 25; Gaps 9.

QY	67	PEDLFMPCFG-----CQC---YSRVVHCSDLGTSVPTNPIDFTRMLDQNNKTK	114
Db	24	PADDYGYDFGFSAVCAPECNCPSLSPYAMDNLKLTPI-VPSGIKYLYLRNMIE	82
QY	115	EIKENDFXGLTSLYGLILNNKL--TKIHPKAFLTTKLRRLYLSHNLQSEIPLNPKSL	172
Db	83	AIEERTFQNVTDQWLILDHNLHNSKIKGRVFSKLNKLUKHINTNUTEAVGPEUPTL	142
QY	173	AERITHENKVKIKODTFKGNNALHIVLEMSANPLDNGIEPGAFGV-TVFHIRAEAKL	231
Db	143	DLQJLSHAKITKVNPALGELVNI-TVTHLQNNOLTKDTSIS-GAFKGLNSLLYLDLSFNOL	201
QY	232	TSVPKGLPTLELHLDYKNKISVELEDBFKRYKELORGLGNKKITDIE--NGLANIPIRV	290
Db	202	TKLPTGLPSSLMLLYFDNNQISNPIDVEYFGQKTLQYLRLSHNLKLTDSGIPGVNITSL	261
QY	291	REIHLNENKLIKIPSGPELK--YLOIIFLHSNISARVGVNDPCPTVPKMKKSLYSATSL	348
Db	262	VELDLSFOLKISITPVSENLENFYQV-----NKINKFPLSFCVKVGLPYTSKITHRL	316
QY	349	FNNPVYKWEQMPATFRCVLSRMSVOL	374
Db	317	DGNNTLRADLPQEMYNCLRVAADISL	342

RESULT 12
A46743
lumican precursor - bovine
N:Alternate names: 37K keratan sulfate-linked protein; corneal keratan sulfate proteo
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999
C:Accession: A46743; A55379
R:K/Funderburgh, J.L.: Funderburgh, M.L.; Brown, S.J.; Vergnes, J.P.; Hassell, J.R.; Ma
J. Biol. Chem. 268, 11874-11880, 1993
A:Title: Sequence and structural implications of a bovine corneal keratan sulfate pro

Search completed: May 27, 2003, 16:05:37
Job time : 24 secs



GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 15:55:26 ; Search time 14 Seconds
(without alignments)
1122.823 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFTS.....PATFRVLSRMSVQLNFCGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Aligned: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1992	100.0	379	1	ASPN_HUMAN	Q9bxn1 homo sapien
2	1799	90.3	373	1	ASPN_MOUSE	Q99mq4 mus musculus
3	1044	52.4	368	1	PGS1_XENLA	Q91b75 xenopus lae
4	1040.5	52.2	369	1	PGS1_RAT	P47853 rattus norv
5	1037.5	52.1	369	1	PGS1_MOUSE	P28653 mus musculus
6	1034	51.9	368	1	PGS1_HUMAN	P21810 homo sapien
7	1028.5	51.6	372	1	PGS1_HORSE	O46403 equus cabal
8	1027.5	51.6	369	1	PGS1_SHEEP	O46390 ovnis aries
9	1021.5	51.3	369	1	PGS1_CANFA	O02678 canis famil
10	1019.5	51.2	369	1	PGS1_BOVIN	P21809 bos taurus
11	974	48.9	356	1	PGS2_COTJA	Q9de68 coturnix co
12	969	48.6	357	1	PGS2_CHICK	P28675 gallus gall
13	967	48.5	360	1	PGS2_PIG	Q9xsd9 sus scrofa
14	963.5	48.4	359	1	PGS2_HUMAN	P07585 homo sapien
15	947	47.5	360	1	PGS2_SHEEP	Q91te2 ovnis aries
16	943	47.3	360	1	PGS2_BOVIN	P21793 bos taurus
17	941	47.2	360	1	PGS2_RABIT	Q28888 eryctolagus
18	939	47.1	360	1	PGS2_HORSE	O46542 equus cabal
19	934	46.9	360	1	PGS2_CANFA	Q29393 canis famil
20	907.5	45.6	354	1	PGS2_MOUSE	P28654 mus musculus
21	899	45.1	354	1	PGS2_RAT	Q01129 rattus norv
22	641	32.2	272	1	PGS1_PIG	Q99kq6 sus scrofa
23	442	22.2	135	1	PGS1_RABIT	O46377 eryctolagus
24	399.5	20.1	343	1	LUM_CHICK	P51890 gallus gall
25	398.5	20.0	343	1	LUM_COTJA	Q9de67 coturnix co
26	390	19.6	338	1	LUM_MOUSE	P51884 homo sapien
27	384	19.3	342	1	LUM_BOVIN	O05443 bos taurus
28	383	19.2	338	1	LUM_MOUSE	P51885 mus musculus
29	378	19.0	338	1	LUM_RAT	P51886 rattus norv
30	366	18.4	421	1	OMD_HUMAN	Q99983 homo sapien
31	363.5	18.2	646	1	FLR3_HUMAN	Q9nzu0 homo sapien
32	361.5	18.1	381	1	PRLP_BOVIN	Q99kn8 bos taurus
33	358.5	18.0	382	1	PRLP_HUMAN	P51888 homo sapien

RESULT 1
ASPN_HUMAN
ID ASPN_HUMAN STANDARD: PRT: 379 AA.
AC Q9BXN1: Q96LD0; Q96K79;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Asporin precursor (periodontal ligament associated protein-1) (PLAP-1).
GN ASPN OR PLAP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITE
RP ASN-281, MASS SPECTROMETRY, AND POLYMORPHISM OF POLY-ASP REGION.
RC TISSUE=Cartilage;
RX MEDLINE=21192276; PubMed=11152692;
RA Lorenzo P., Aspberg A., Oennerfjord P., Bayliss M.T., Neame P.J.,
RA Heinegaard D.;
RT "Identification and characterization of asporin. A novel member of the
RT leucine-rich repeat protein family closely related to decorin and
RT biglycan.";
J. Biol. Chem. 276:12201-12211(2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21472263; PubMed=11587855;
RA Yamada S., Murakami S., Matoba R., Ozawa Y., Yokokoji T., Nakahira Y.,
RA Ikezawa K., Takayama S.-I., Matsubara K., Okada H.;
RT "Expression profile of active genes in human periodontal ligament and
RT isolation of PLAP-1, a novel SLRP family gene.";
Gene 275:279-286(2001).
[3]
RP SEQUENCE OF 1-242 FROM N.A.
RC TISSUE=Embryo;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wadatsuma T., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NED0 human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[4]
RP PARTIAL SEQUENCE FROM N.A.
RX PubMed=11152695;
RA Henry S.P., Takanosu M., Boyd T.C., Mayne P.M., Eberspaecher H.,
RA Zhou W., de Crombrughe B., Hoeck M., Mayne R.;
RT "Expression pattern and gene characterization of asporin. A newly
RT discovered member of the leucine-rich repeat protein family.";
J. Biol. Chem. 276:12212-12221(2001).
RL J. Biol. Chem. 276:12212-12221(2001).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix.
CC -!- TISSUE SPECIFICITY: Higher levels in osteoarthritic articular
CC cartilage, aorta, uterus. Moderate expression in small intestine.

ALIGNMENTS

34	356.5	17.9	377	1	PRLP_RAT	Q9eqp5 rattus norv
35	345	17.3	351	1	KERA_MOUSE	O35367 mus musculus
36	342.5	17.2	375	1	FMOD_BOVIN	P13605 bos taurus
37	342.5	17.2	378	1	PRLP_MOUSE	O91k53 mus musculus
38	340.5	17.1	352	1	KERA_BOVIN	O62702 bos taurus
39	340.5	17.1	352	1	KERA_HUMAN	O60938 homo sapien
40	338	17.0	376	1	FMOD_RAT	P50609 rattus norv
41	338	17.0	422	1	OMD_BOVIN	O77742 bos taurus
42	333.5	16.7	380	1	FMOD_CHICK	P51887 gallus gall
43	331.5	16.6	649	1	FLR3_HUMAN	Q9nzu0 homo sapien
44	331	16.6	376	1	FMOD_MOUSE	P50608 mus musculus
45	325	16.3	353	1	KERA_CHICK	O42235 gallus gall


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CC -----
DR EMBL: AB037269; BAA90246.1; -
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_Out.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam: PF00560; LRR. 9.
DR Pfam: PF01462; LRRNT. 1.
DR SMART: SM00370; LRR. 1.
DR SMART: SM00013; LRRNT. 1.
DR SMART: SM00369; LRR_Typ. 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 ? BY SIMILARITY.
FT CHAIN 63 76 BIGLYCAN.
FT DOMAIN 82 102 CYS-RICH.
FT REPEAT 82 102 LRR-S 1.
FT REPEAT 103 126 LRR-T 1.
FT REPEAT 127 150 LRR-T 2.
FT REPEAT 151 171 LRR-S 2.
FT REPEAT 172 195 LRR-T 3.
FT REPEAT 196 220 LRR-T 4.
FT REPEAT 221 241 LRR-S 3.
FT REPEAT 242 265 LRR-T 5.
FT REPEAT 266 289 LRR-T 6.
FT REPEAT 290 312 LRR-S 4.
FT REPEAT 313 342 LRR-T 7.
FT REPEAT 343 368 LRR-T 8.
FT DISULFID 63 76 BY SIMILARITY.
FT DISULFID 321 354 BY SIMILARITY.
SQ SEQUENCE 368 AA; 41197 MW; 53ADF7E7E3BDC528 CRC64;

Query Match 52.4%; Score 1044; DB 1; Length 368;
Best Local Similarity 58.18; Pred. No. 3.3e-65;
Matches 193; Conservative 61; Mismatches 72; Indels 6; Gaps 3;

QY 49 DEDNSL--FTTRE--PRGHFFPDLFPMPCGOCYSRVHCSDGLTSTVPTNIPFDTRM 105
Db 38 DEASGVGPPTESIPDVGLPMDL--CPGCGCHLRVQVCSGLTSTPKNLPKDTTL 94
QY 106 LDQNNKKEIKENDFKGLTSLYLGLNNKLTIKHPKAFITTKRLRYLSHNLSEIP 165
Db 95 LDQNNKITEIKKDFKGLTSLYLGLNNKLTIKHPKAFITTKRLRYLSHNLSEIP 154
QY 166 LNLPSLAELRIHENKVKIKQDFKGNALHLEMSANPLDNNNGIECPAEGVTVEHIR 225
Db 155 KNLPSLVELRIHENKIKKVPKGVSGLNKNCNTEMGNPLENGIEAGAFDGLKLYLR 214
QY 226 TAAKLTSPKGLPTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNKKTIDENGSLA 285
Db 215 VSEAKLSGIPKGLPTLLEHLHDNKNKIQAEKEDLSQVASYRLGLGHNNTRMTENGSL 274
QY 286 NTPRVREHLENNKIKKTPSGLPKLYLIQIFLHNSNARVGVNDFCPTVPKMKSLYSA 345
Db 275 FMPVLRELHLDNNKLSKVPKGLPMDKLVYLLHNSNITQVGVNDFCPTVPKMKSLY 334
QY 346 ISLFNNPKYKEMQATPCRCVLSRMSVOLGNF 377
Db 335 ISLFNNPKYKEMQATPCRCVLTDLAIOGNY 366

RESULT 4
PGSI_RAT STANDARD; PRT; 369 AA.
AC P47853;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan 1) (PG-S1).
GN BGN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RX TISSUE=Vascular smooth muscle;
RX MEDLINE=91184222; PubMed=2081545;
RA Dreher K.L., Asundi V.K., Matzura D., Cowan K.;
RT "Vascular smooth muscle biglycan represents a highly conserved
RT proteoglycan within the arterial wall.";
RL Eur. J. Cell Biol. 53:296-304(1990).
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY, CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC
CC EMBL: U17834; AAA58797.1; -
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000372; LRR_Nterm.
CC InterPro: IPR003592; LRR_Out.
CC InterPro: IPR003591; LRR_Typ.
CC Pfam: PF00560; LRR. 8.
CC Pfam: PF01462; LRRNT. 1.
CC SMART: SM00370; LRR. 3.
CC SMART: SM00013; LRRNT. 1.
CC SMART: SM00369; LRR_Typ. 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 37 BIGLYCAN.
FT CHAIN 38 369 CYS-RICH.
FT DOMAIN 64 77 LRR-S 1.
FT REPEAT 83 103 LRR-T 1.
FT REPEAT 104 127 LRR-T 2.
FT REPEAT 128 151 LRR-S 2.
FT REPEAT 152 172 LRR-T 3.
FT REPEAT 173 196 LRR-T 4.
FT REPEAT 197 221 LRR-S 3.
FT REPEAT 222 242 LRR-T 5.
FT REPEAT 243 266 LRR-T 6.
FT REPEAT 267 290 LRR-S 4.
FT REPEAT 291 313 LRR-T 7.
FT REPEAT 314 343 LRR-T 8.
FT REPEAT 344 369 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT CARBOHYD 42 42 SIMILARITY).
FT CARBOHYD 48 48 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT CARBOHYD 271 271 SIMILARITY).
FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 64 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 322 355 BY SIMILARITY.
SQ SEQUENCE 369 AA; 41706 MW; 319DC15117F2C604 CRC64;

Query Match 52.2%; Score 1040.5; DB 1; Length 369;
Best Local Similarity 52.6%; Pred. No. 5.7e-65;
Matches 199; Conservative 67; Mismatches 93; Indels 19; Gaps 3;
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QY 4 YVLLFLALCSAKPF-----FSPSHIALKNMMLKOWEDTDDDDDDDDDDDDDDDDDDNSLPFTR 59
 Db 5 WLLTLLALLSQAALPEQKGFWDFTLDDGLLMMNDEEASGSDTTSVDPDL-----SLPPT- 59
 QY 60 EPRSHFFPDLFPWCPFCOCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEKEN 119
 Db 60 -----FSAMCPFGCHLRRVQCSDLGLTVKPREISPDFTLDDLQNNDTSELKRD 109
 QY 120 DFKGLTSLYGLILNKKLTIKHPKAFLTTRKRLYLKSHNOLSEIPLNPKSLAEIRHE 179
 Db 110 DFKGLHLYALVNNKISKIHERAFSPRLKQLYISKHNLVEIPNLSLVELRIHD 169
 QY 180 NKVKIKODTFKGNALHVLMSANPLDNGIEPAGFEGVTVFHRTAEAKLTSVPKGLP 239
 Db 170 NRIRKRVGVSGLRNNCIEMGNPLNSGFEFGAPDGLKLYRLTSEAKLTGPKDLP 229
 QY 240 PTLEHLHDYKNISTVELEDFKRYKELQRLGLGNKTKTDITENGLANIPIVREIHLNKK 299
 Db 230 ETNELHLDHKNKIQAELEDLLRYSKLYRGLGHQNTMTENGSLPFLPTRELHLDNNK 289
 QY 300 LKKTIPSGLPKLYLOITFLHNSNISTARVGVNDPCTVPEKMKKSLYSALSIFNPNPVKWMQ 359
 Db 290 LSRVPAGLPDLKLVYLLSHNNITKVGINDFCPMGFGVKRAYNGISLIFNPNPVYWEQ 349
 QY 360 PATRCVLSRMSVOLGNF 377
 Db 350 PATRCVTDRLAQFGNY 367
 RESULT 5
 PGSI_MOUSE
 ID PGSI_MOUSE STANDARD; PRT; 369 AA.
 AC P28653; Q61355;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan 1) (PG-S1).
 GN BGN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss; TISSUE=Fibroblast;
 RC Naithoh Y., Suzuki S.;
 RN Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss; TISSUE=Embryo;
 RC MEDLINE=94319093; PubMed=8043960;
 RA Rau W., Just W., Vetter U., Vogel W.;
 RT "A dinucleotide repeat in the mouse biglycan gene (EST) on the X
 RT chromosome.";
 RL Mamm. Genome 5:395-396(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Breast, and Kidney;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE OF 11-152 FROM N.A.
 RC STRAIN=C57BL/6;
 RC PubMed=11311118;
 RA Saeemaenen A.-M.K., Salminen H.J., Rantakokko A.J., Heinigaard D.,
 RA Vuorio E.I.;
 RT "Murine fibromodulin: cDNA and genomic structure, and age-related
 RT expression and distribution in the knee joint.";
 RL Biochem. J. 355:577-585(2001).
 CC -!- FUNCTION: May be involved in collagen fiber assembly (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially

CC in articular cartilages.
 CC -!- PTM: The two attached glycosaminoglycan chains can be either
 CC chondroitin sulfate or dermatan sulfate (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPS) FAMILY. CLASS I SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC
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 CC
 CC EMBL; X53928; CAA37875.1; -;
 CC EMBL; L20276; AAA64360.1; -;
 CC EMBL; BC005452; AAH05452.1; -;
 CC EMBL; BC019502; AAH19502.1; -;
 CC EMBL; Y11758; CAA72422.1; -;
 CC PIR; S20811; S20811.
 CC MGD; MGI:88158; Bgn.
 CC InterPro; IPR001611; LRR.
 CC InterPro; IPR000372; LRR Nterm.
 CC InterPro; IPR003592; LRR Out.
 CC InterPro; IPR003591; LRR typ.
 CC Pfam; PF00560; LRR; 8.
 CC Pfam; PF01462; LRRNT; 1.
 CC SMART; SM00370; LRR; 3.
 CC SMART; SM00013; LRRNT; 1.
 CC SMART; SM00369; LRR_TYP; 1.
 CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal. POTENTIAL.
 FT SIGNAL 1 19
 FT PROPEP 20 37
 FT CHAIN 38 369
 FT DOMAIN 64 77
 FT REPEAT 83 103
 FT REPEAT 104 127
 FT REPEAT 128 151
 FT REPEAT 152 172
 FT REPEAT 173 196
 FT REPEAT 197 221
 FT REPEAT 222 242
 FT REPEAT 243 266
 FT REPEAT 267 290
 FT REPEAT 291 313
 FT REPEAT 314 343
 FT REPEAT 344 369
 FT CARBOHYD 42 42
 FT CARBOHYD 48 48
 FT CARBOHYD 271 271
 FT CARBOHYD 312 312
 FT DISULFID 64 77
 FT DISULFID 322 355
 FT CONFLICT 68 68
 FT CONFLICT C -> W (IN REF. 2).
 SQ SEQUENCE 369 AA; 41639 MW; 4B57FCC9A1026BE6 CRC64;
 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 SIMILARITY).
 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 SIMILARITY).
 N-LINKED (GLCNAC. .) (POTENTIAL).
 N-LINKED (GLCNAC. .) (POTENTIAL).
 BY SIMILARITY.
 BY SIMILARITY.
 C -> W (IN REF. 2).
 Query Match 52.1%; Score 1037.5; DB 1; Length 369;
 Best Local Similarity 52.4%; Pred. No. 9.2e-65;
 Matches 198; Conservative 68; Mismatches 93; Indels 19; Gaps 3;
 QY 4 YVLLFLALCSAKPF-----FSPSHIALKNMMLKOWEDTDDDDDDDDDDDDDDDDDDNSLPFTR 59
 Db 5 WLLTLLALLSQAALPEQKGFWDFTLDDGLLMMNDEEASGSDTTSVDPDL-----SLPPT- 59
 QY 60 EPRSHFFPDLFPWCPFCOCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEKEN 119
 Db 60 -----FSAMCPFGCHLRRVQCSDLGLTVKPREISPDFTLDDLQNNDTSELKRD 109
 QY 120 DFKGLTSLYGLILNKKLTIKHPKAFLTTRKRLYLKSHNOLSEIPLNPKSLAEIRHE 179

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Db 110 DFKGLQHLVALVNNKISKITHKAFSPRLKLOKLYTSKNHLVPEIPNLPSSUVELRIHD 169
Qy 180 NKVKIKQIDTFKGMNALHVLMSANPLDNNNGIEPCAFEGVTVFHRIARAEAKLTSPVKGLP 239
Db 170 NKIRKVPKVSGLRNMNCIEMGNGPLENSGFPCAFDGLKLYLRISAKLTGIPKDLPL 229
Qy 240 PTLLEHLHDYKNIKISTVELEDPKRYKELQRLGLGNKKITFDIENGSLANIIPRVREIHLNNK 299
Db 230 ETLNELHLHDHKKIQATELEDLLRYLSKLYRLGLGHQIRMIENGSLSFLEPTRELHLNNK 289
Qy 300 LKKIPSGPELKYLOIIFLHNSIARVNDPCPTVPKWKKSLSYATSLSFNPNPKYWEQ 359
Db 290 LSRVAGLUPDLKLLQVYLHNSNITKVGINDPCPMGFCVKRAYNGISLFNPNPKYWEQ 349
Qy 360 PATFRCLVLSRMSVQLGNF 377
Db 350 PATFRCLVLSRMSVQLGNF 367

RESULT 6
PGS1_HUMAN
P21810: P13247: STANDARD: PRT: 368 AA.
01-JAN-1990 (Rel. 13, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-SL).
GN - BGN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN - [1]
SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=89174714; PubMed=2647739;
RA Fisher L.W., Termine J.D., Young M.F.;
RT "Deduced protein sequence of bone small proteoglycan I (biglycan)
RT shows homology with proteoglycan II (decorin) and several
RT nonconnective tissue proteins in a variety of species."
RL J. Biol. Chem. 264:4571-4576(1989).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=91317791; PubMed=1860845;
RA Fisher L.W., Heegaard A.M., Vetter U., Vogel W., Just W.,
RA Termine J.D., Young M.F.;
RT "Human biglycan gene. Putative promoter, intron-exon junctions, and
RT chromosomal localization."
RL J. Biol. Chem. 266:14371-14377(1991).
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=20314869; PubMed=10854409;
RA Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
RA Nordstrek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
RA Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K.,
RA Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,
RA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man."
RL Genome Res. 10:758-775(2000).
RN [4]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
SEQUENCE OF 38-57.
RX MEDLINE=90073579; PubMed=2590169;
RA Roughley P.J., White R.J.;
RT "Dermatan sulphate proteoglycans of human articular cartilage. The
RT properties of dermatan sulphate proteoglycans I and II."

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RL Biochem. J. 262:823-827(1989).
RN [6]
RP SEQUENCE OF 38-66.
RX MEDLINE=87250639; PubMed=3597437;
RA Fisher L.W., Hawkins G.R., Tuross N., Termine J.D.;
RT "Purification and partial characterization of small proteoglycans I
RT and II, bone sialoproteins I and II, and osteonectin from the mineral
RT compartment of developing human bone."
RL J. Biol. Chem. 262:9702-9708(1987).
RN [7]
RP SEQUENCE OF 361-368 FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=95187185; PubMed=7881444;
RA Just W., Rau W., Muller R., Geerckens C., Vogel W.;
RT "Dinucleotide repeat polymorphism at the human biglycan (BGN)
RT locus."
RL Hum. Mol. Genet. 3:2268-2268(1994).
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
CC similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
CC in articular cartilages.
CC -!- PTM: The two attached glycosaminoglycan chains can be either
CC chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SLRPS) FAMILY. CLASS 1 SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
CC EMBL: J04599; AAA36009.1; -
CC EMBL: M65153; AAA52287.1; ALT_SEQ.
CC EMBL: M65152; AAA52287.1; JOINED.
CC EMBL: U82695; AAF33530.1; -
CC EMBL: BC002416; AAH02416.1; -
CC EMBL: BC004244; AAH04244.1; -
CC EMBL: U11686; AAC50117.1; -
CC PIR: A28457; A28457.
CC PIR: A32458; A32458.
CC PIR: A40757; A40757.
CC PIR: S05639; S05639.
CC Genew: HGNC:1044; BGN.
CC MIM: 301870; -
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000372; LRR_Nterm.
CC InterPro: IPR003592; LRR_out.
CC InterPro: IPR003591; LRR_typ.
CC Pfam: PF00560; LRR: 8.
CC Pfam: PF01462; LRRNT; 1.
CC SMART: SM00370; LRR: 3.
CC SMART: SM00013; LRRNT; 1.
CC SMART: SM00369; LRR_TYP; 1.
CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19
FT PROPEP 20 37
FT CHAIN 38 368
FT DOMAIN 63 76
FT REPEAT 82 102
FT REPEAT 103 126
FT REPEAT 127 150
FT REPEAT 151 171
FT REPEAT 172 195
FT REPEAT 196 220
FT REPEAT 221 241

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[illegible]

RESULT	7	PGSL_HORSE	STANDARD;	PRT;	372 AA.
ID	PGSL_HORSE	STANDARD;	PRT;	372 AA.	
AC	046403;	09NIU5;			
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DE	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Biglycan precursor	(Bone/cartilage proteoglycan I) (PG-SI).			
GN	BGN.				
OS	Equus caballus (Horse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				
OX	NCBI_TaxID=9796;				
[1]					
SEQUENCE FROM N.A.					
Richardson D.W., Dodge G.R.;					
"dose dependent effects of corticosteroids on the expression of matrix					
related genes in equine articular chondrocytes.";					
Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.					
[2]					
SEQUENCE OF 150-192 FROM N.A.					
MEDLINE=20082971; PubMed=10613847;					
Caetano A.R., Shlue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,					
Bowling A.T., Murray J.D.;					
"A comparative gene map of the horse (Equus caballus).";					

Genome Res. 9:1239-1249(1999).

-!- FUNCTION: May be involved in collagen fiber assembly (By similarity).

-!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By similarity).

-!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity). chondroitin sulfate or dermatan sulfate chain can be either (SURPS) FAMILY. CLASS I SUBFAMILY.

-!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).

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EMBL; AF035934; AAB88305.1; -.
EMBL; AF135020; AAF64248.1; -.
InterPro: IPR001611; LRR.
InterPro: IPR000372; LRR_Nterm.
InterPro: IPR003592; LRR_Out.
Pfam; PF00560; LRR; 7.
Pfam; PF01462; LRRNT; 1.
SMART; SM00370; LRR; 3.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_Typ; 1.
GlycoProtein; Extracellular matrix; Proteoglycan; Repeat;
Leucine-rich repeat; Signal.
SIGNAL 1 22 POTENTIAL
FT PROPEP 23 40 BY SIMILARITY.
FT CHAIN 41 372 CYS-GLYCAN.
FT DOMAIN 67 80 BICYCLIN.
FT REPEAT 86 106 LRR-S 1.
FT REPEAT 107 130 LRR-T 1.
FT REPEAT 131 154 LRR-T 2.
FT REPEAT 155 175 LRR-S 2.
FT REPEAT 176 199 LRR-T 3.
FT REPEAT 200 224 LRR-T 4.
FT REPEAT 225 245 LRR-S 3.
FT REPEAT 246 269 LRR-T 5.
FT REPEAT 270 293 LRR-T 6.
FT REPEAT 294 316 LRR-S 4.
FT REPEAT 317 346 LRR-T 7.
FT REPEAT 347 372 LRR-T 8.
FT CARBOHYD 45 45 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT FT 51 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 67 80 BY SIMILARITY.
FT DISULFID 325 358 BY SIMILARITY.
SQ SEQUENCE 372 AA; 41924 MW; D0BBE8576C5F082E CRC64;

Query Match 51.6%; Score 1028.5; DB 1; Length 372;
Best Local Similarity 52.4%; Pred. No. 3.9e-64;
Matches 198; Conservative 67; Mismatches 94; Indels 19; Gaps 3;

QY 4 YVLLFLALCAKPF----FSPSHIALKNMKLDWETDDDDDDDDDDDDDDSDSLFPFR 59
: : | | | | | : : : : : | | | | | : : : : :
Db 8 WLLASLLALSOALPPFQKGFWDFTLDDGLPLMDEAGADTSIGIPDL-----SLTPT- 62

QY 60 EPRAHFFFDLPFCMPFGCCQSYRVVHCSDLGTVPTNPFDTRMLDLQNKKI KEIKEN 119
| | | | | : : : : : | | | | | : : : : :
Db 63 -----FSAMCPFGCHLRVVQCSDLGKAVPKREISPDITLLDLQNETSELRKD 112

QY 120 DKGLGTSYLGLTNLNKLTKIHKFAFLTTKLRRRLYLSHNOLSEIPLNPKSLAEIRIE 179
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

Db	113	DFKGLQHLVALVLVNKKISKIHEKAFSPURKQLQKLYISKNHVLVIPPPLSSSLVELRIHD	172
Qy	180	NKVKKIOKDTKGMNAHLVLEMSANPLDNGTEPGAFEGVTVFHRTAEAKLTSPVKGLP	239
Db	173	NRIRKPVGVSGLRNWNCLEMGNPLENSGPOGAFDGLKLYLRSEAKLTGIPKDL P	232
Qy	240	PTLLEHLHDYKNKISTVELEDFKRYQLORGLGNKKITDIENGSLANI PVR EHLHLENNK	299
Db	233	ETLNEHLHDHNKIOAIELEDLLRYSKLYRLGLGCHQIRMIENGSLSFUPTLRELHLDNKK	292
Qy	300	LKKIPSGPELKYLOITFLHSNSTARVGNDFCPTVPKMKKSLXSAISLFNNPVKVMQ	359
Db	293	LSRPVAGUPDUKLQVYVLTNNITKVGNDFCVPGCFGVKRAYINGISLFNNPVYWEVQ	352
Qy	360	PATFCRCVLSRMSVQLGNF	377
Db	353	PATFCVTDRLAIOFGNY	370

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RESULT 8
PGSL_SHEEP
ID PGSL_SHEEP STANDARD; PRNT; 369 AA.
O46390;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).
GN BGN.
OS - Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Choroid plexus;
RA Bruett L., Clements J.E.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be involved in collagen fiber assembly (By
similarity).
CC -!- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Found in several connective tissues, specially
in articular cartilages.
CC -!- PTM: the two attached glycosaminoglycan chains can be either
chondroitin sulfate or dermatan sulfate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
(SLRPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).

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CC EMBL; AF034842; AAB87988.1; --
DR InterPro; IPR0001611; LRR.
DR InterPro; IPR0003772; LRR_Nterm.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003591; LRR_type.
DR Pfam; PF00560; LRR; 7.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 3.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_type; 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 37 BY SIMILARITY.

FT	CHAIN	38	369	BIGLYCAN.
FT	DOMAIN	64	777	CYS-RICH.
FT	REPEAT	83	103	LRR-S 1.
FT	REPEAT	104	127	LRR-T 1.
FT	REPEAT	128	151	LRR-T 2.
FT	REPEAT	152	172	LRR-S 2.
FT	REPEAT	173	196	LRR-T 3.
FT	REPEAT	197	221	LRR-T 4.
FT	REPEAT	222	242	LRR-S 3.
FT	REPEAT	243	266	LRR-T 5.
FT	REPEAT	267	290	LRR-T 6.
FT	REPEAT	291	313	LRR-S 4.
FT	REPEAT	314	343	LRR-T 7.
FT	REPEAT	344	369	LRR-T 8.
FT	CARBOHYD	42	42	O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT	CARBOHYD	48	48	O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT	CARBOHYD	271	271	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	312	312	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	64	77	BY SIMILARITY.
FT	DISULFID	322	355	BY SIMILARITY.
FT	SEQUENCE	369	AA: 415232	048C82C233909EE6 CRC64;

[illegible]

RESULT 9					
PGS1_CANFA					
ID	PGS1_CANFA	STANDARD:	PRT:	369 AA.	
AC	002678:				
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Biglycan precursor (Bone/cartilage proteoglycan I) (PG-S1).				
GN	BGN.				
OS	Canis familiaris (Dog).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
OX	NCBI_TaxID=9615;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Glant T.T.;				

[illegible]

CC chondroitin sulfate or dermatan sulfate.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SURPS) FAMILY. CLASS 1 SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S82652; AAB46746.2; -
 DR PIR: A33701; A33701. LRR.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_typ.
 DR Pfam: PF00560; LRR: 7.
 DR Pfam: PF01462; LRRNT: 1.
 DR SMART: SM00370; LRR: 3.
 DR SMART: SM00013; LRRNT: 1.
 DR SMART: SM00369; LRR_TYP: 1.
 DR Glycoprotein; Extracellular matrix; Proteoglycan; Signal; Repeat;
 KW Leucine-rich repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 37
 FT CHAIN 38 369
 FT DOMAIN 64 77
 FT REPEAT 83 103
 FT REPEAT 104 127
 FT REPEAT 128 151
 FT REPEAT 152 172
 FT REPEAT 173 196
 FT REPEAT 197 221
 FT REPEAT 222 242
 FT REPEAT 243 266
 FT REPEAT 267 290
 FT REPEAT 291 313
 FT REPEAT 314 343
 FT REPEAT 344 369
 FT CARBOHYD 42 48
 FT CARBOHYD 48 48
 FT CARBOHYD 271 271
 FT CARBOHYD 312 312
 FT DISULFID 64 77
 FT DISULFID 322 355
 FT CONFLICT 152 152
 FT CONFLICT 188 188
 FT CONFLICT 354 354
 FT CONFLICT 368 369
 FT SEQUENCE 369 AA; 41509 MW; 453309FFBD1B8872 CRC64;
 Query Match 51.2%; Score 1019.5; DB 1; Length 369;
 Best Local Similarity 51.9%; Pred. No. 1.6e-63;
 Matches 195; Conservative 65; Mismatches 97; Indels 19; Gaps 3;
 QY 6 LLLFLALCSAKPFPSHTALKNMKMDTDDDD-----DDDDDDDDDDNSLFTREP 61
 Db 7 LAALLALSQLPFEQ-----KAFWFTLDDGLPMLNDEEASGAFTTSGIPDLDS 55
 QY 62 RSHFFPDLFPMPGFCQCYSRVVHSCDGLGTSVPTNIPDFTPMLDLQNNKKEIKENDF 121
 Db 56 -----LPPTYSAMCPFGCHCHLRVQCSGLGKAVKPEISPDFTLLDQNNIDSELKDDF 111
 QY 122 KGLTSLGLTLNKNKTKIHPKAFITTKLRLRLYLSHNSOLSEIPLNPKSLAELRIHKNK 181
 Db 112 KGLQHLVTLVNNKISKIIEHKAFLSPKQKLYISKNHLCETPPNLPSSLVELRIHDNR 171
 QY 182 VKTIQKDTFKGMNALHVLSEANPLDNNNGIEGAFGVTVFHTRIAEAKITSVPGKLPPT 241
 Db 172 IRKVPKGVFSLGRNMNCIENGNGNPLENSGPEGAFGLKLNLYRISAEKITGIPKLPET 231

QY 242 LLEHLHDYKRIKSTIVELEDFKRYKEIQRLGLGNKKITDIENGSLANIPKRVREITHLNNK 301
 Db 232 LNELHLHDHKNKIAIELEDFLRYSKLYRLGLGHQIRMIENGSLFLPTRELHLDNNKLS 291
 QY 302 KIPSGLPKLYLIQILFELHNSLARVCVNDPCPTVPMKKSLSYSAISLNNPKYKYMOP 361
 Db 292 RVPAGLPDLKLLQVYVLTNNITKGVNDPCPVGVCKRAYNGISLNNPVPYVEVQPA 351
 QY 362 TPRCVLSRMSVOLGNF 377
 Db 352 TFACVTDRLAIQFNY 367
 RESULT 11
 PGS2_COTJA STANDARD; PRT; 356 AA.
 AC QDE68;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Decorin precursor (Bone proteoglycan II) (PG-S2).
 GN DGN.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Coturnix.
 OC NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Cornea, and Sclera;
 RX MEDLINE=20556471; PubMed=11102759;
 RA Corpuz L.M., Dunlevy J.R., Hassell J.R., Conrad A.H., Conrad G.W.;
 RT "Molecular cloning and relative tissue expression of decorin and
 lumican in embryonic quail cornea";
 RL Matrix Biol. 19:699-704(2000).
 CC -!- FUNCTION: May affect the rate of fibrils formation (By
 CC similarity).
 CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
 CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
 CC -!- PTM: The attached glycosaminoglycan chain can be either
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue
 CC of origin (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SURPS) FAMILY. CLASS 1 SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF125250; AAG48154.1; -
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR003591; LRR_typ.
 DR Pfam: PF00560; LRR: 10.
 DR Pfam: PF01462; LRRNT: 1.
 DR SMART: SM00370; LRR: 3.
 DR SMART: SM00013; LRRNT: 1.
 DR SMART: SM00369; LRR_TYP: 7.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 FT SIGNAL 1 15 POTENTIAL.
 FT PROPEP 16 29
 FT CHAIN 30 356
 FT DOMAIN 51 64

RT proteoglycan reveals identity to decorin.";

125 TSLYGLIINNKKLTKIHPKAFLTTKKLRRLYLSHINOLSEIPLNLPKSIAEIRIHENKVVK 184

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Db 103 KNLHALILVNNKISKTSAPAFAPLKKLERLYLSKNKLKELPENMPKSLQETIRAHENEISK 162
QY 185 IOKDTFGKGNALHVLMSANPLDNNNGIEPGAFGV-TVFHRIABAKLTSVPGKGLPPTIL 243
Db 163 LRAVANGLNQVIVLELGNPLKSSGIEGAFQGMKRLSYIRIADNTITSIPKGLPPSIT 222
QY 244 ELHLDYKNTSTVELEDFKRYKELQRLGLGNKNTIDTENGSLANIPRVREIHLNKKLKI 303
Db 223 ELHLDGCKISKIDAEGSLGTLNKLKGLSFNSTSSVGENSLNNVPHRLHLLHNNELVRV 282
QY 304 PSGLPKLYLQIIFLHNSNARVGVNDPCTVPKMKKSLYSALSIFNNPVKYWQOPATF 363
Db 283 PSGLGEHKYIQVYVYLNHNKIAGINDPCPLGYNTRKATYSGVSLFSNPVQIWEIQPSAF 342
QY 364 RCVLSRMSVOLGNF 377
Db 343 RCIHERSAVOIGNY 356

RESULT 13
PGS2_PIG STANDARD: PRT: 360 AA.
O9XSD9: O9XSH4;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
GN DGN.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A. (LONG ISOFORM).
STRAIN=Yorkshire;
Stephenson S., Schnoke M., Vesely I.;
"Cloning of the porcine decorin gene.";
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
SEQUENCE FROM N.A. (SHORT ISOFORM).
STRAIN=Yorkshire; TISSUE=Aorta;
Stephenson S., Schnoke M., Vesely I.;
"Alternately spliced version of the porcine decorin gene.";
Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -!- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular matrix (By similarity).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here)
CC and a short form; are produced by alternative splicing.
CC -!- PM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC (SURPS) FAMILY. CLASS I SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF125537; AAD23578.1; .
CC EMBL; AF140270; AAD33862.1; .
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003592; LRR_out.

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DR InterPro: IPR003591; LRR_typ.
DR Pfam; PF00560; LRR; 7
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00370; LRR; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 2.
KW Glycoprotein; Extracellular matrix; proteoglycan; Repeat;
KW Leucine-rich repeat; Signal; Alternative splicing.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 314 347
FT CARBOHYD 34 34
FT CARBOHYD 212 212
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT VARSPLIC 281 318
SQ SEQUENCE 360 AA; 39899 MW; 8573DE8DDEBA7509 CRC64;

Query Match 48.5%; Score 967; DB 1; Length 360;
Best Local Similarity 50.9%; Pred. No. 6.6e-60;
Matches 193; Conservative 63; Mismatches 101; Indels 22; Gaps 5;

QY 1 MKEYVLLFLALCS-AKPFPSHIALNNMLKMDTDDDDDDDDDDDDDDDDDDDDDDSLFTR 59
Db 1 MKATIVFLLLAQVSWAGPF---QQKGLDFMLEASGIGPEDREPE-----VPEL 48
QY 60 EPRSHPFFPDLFPMCFGCOCYSRVVHCSDLGTSVPTNIPDTRMLDLQNNKIKEIKEN 119
Db 49 EP-----LQPMCFRCQCHLRVQVCSGLGDKVPKDLPDPTALLDLQNNKITEIKDG 100
QY 120 DFKGLTSLYGLILNKNKUTKIHPKAFITTKLRRYLHSHNQSLSEIPLNLPKSLAELRIHE 179
Db 101 DFKNLKLNHTLILINNISKISPGAFAPLVKLERLYLSKNQLKELPEKMPKTLQELRYHE 160
QY 180 NKVKKTKQDTFKGMNALHYLEMSANPLDNNNGIEPGAFGV-TVFHRIABAKLTSVPGKL 238
Db 161 NEITKVRKAVFNLGNOMIVVELGTNPLKSSGIEGAFQGMKRLSYIRIADNTITTIPOGL 220
QY 239 PPTLLEHLDYKNTSTVELEDFKRYKELQRLGLGNKNTIDTENGSLANIPRVREIHLNEN 298
Db 221 PPSLTELHLDGCKISKIDAEGSLGTLNKLKGLSFNSTSSVGENSLNNVPHRLHLLHNN 280
QY 299 KLKIPSGLPKLYLQIIFLHNSNARVGVNDPCTVPKMKKSLYSALSIFNNPVKYWEM 358
Db 281 KLNKVPGLGAEHKYIQVYVYLNHNKIAGINDPCPLGYNTRKATYSGVSLFSNPVQIWEI 340
QY 359 QPATFRCVLSRMSVOLGNF 377
Db 341 QPSTFRFCVYVRSALQLGNY 359

RESULT 14
PGS2_HUMAN STANDARD: PRT: 359 AA.
ID PGS2_HUMAN
AC P07585; O9Y5N9; O9Y5N8; Q9P0Z0; Q9P0Z1;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)

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OM protein - protein search, using sw model

Run on: May 27, 2003, 15:46:26 ; Search time 37 Seconds
(without alignments)
1364.919 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFES.....PATFRCLVLSVQLGNFCM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1992	100.0	379	21	Human PRO241 polyp
2	1992	100.0	379	22	Human PRO241 polyp
3	1992	100.0	379	23	Human angiogenesis
4	1992	100.0	379	23	Human PRO241 prote
5	1990	99.9	379	20	Human PRO241 prote
6	1799	90.3	373	22	Mouse bone/cartila
7	1799	90.3	373	23	Murine protein iso
8	1649	82.8	373	23	Human polypeptide
9	1558	78.2	352	22	Novel human diagno
10	1237	62.1	246	22	Human protein sequ

11	1040.5	52.2	369	16	AA87951	Rat neurotrophic b
12	1034	51.9	368	22	AA85043	Human biglycan pro
13	1031.5	51.8	369	16	AA87952	Human neurotrophic
14	1021	51.3	368	22	AA879510	Human biglycan ami
15	1020	51.2	368	11	AA805159	Sequence of human
16	1015	51.0	332	16	AA87953	Bovine neurotroph
17	1007	50.6	197	22	AA842137	Human polypeptide
18	963.5	48.4	359	21	AA57079	Human decorin amin
19	963.5	48.4	359	22	AA879511	Human decorin amin
20	963.5	48.4	360	22	AA87286	Novel central nerv
21	949	47.6	342	17	AA89439	Human recombinant
22	947	47.5	331	14	AA84260	Mature decorin PT-
23	947	47.5	1388	17	AA89471	Collagen/decorin f
24	947	47.5	1388	21	AA84539	Amino acid sequenc
25	907	45.5	353	11	AA805160	Sequence of human
26	847	42.5	305	14	AA842267	Decorin sequence p
27	793.5	39.8	423	22	AAU30348	Novel human secret
28	776	39.0	280	14	AA842266	Decorin sequence p
29	643	32.3	128	22	AAU20404	Human secreted pro
30	616	30.9	234	14	AA842265	Decorin sequence p
31	493	24.7	88	21	AA800241	Human secreted pro
32	493	24.7	88	21	AA84720	Human 5' EST relat
33	493	24.7	186	14	AA842264	Decorin sequence p
34	433	21.7	146	20	AA59749	Human normal ovari
35	406.5	20.4	155	21	AA844116	Human cancer ovari
36	397.5	20.0	699	21	AA67598	Human adipose tiss
37	393	19.7	353	21	AA843535	Human cancer assoc
38	390	19.6	338	23	ABB90763	Human Tumour Endot
39	390	19.6	353	22	AA873881	Human colon cancer
40	384.5	19.3	139	14	AA842263	Decorin sequence p
41	366	18.4	421	20	AA505767	Human osteomodulin
42	366	18.4	421	21	AA833417	Human PRO216 prote
43	366	18.4	421	21	AA824435	Human PRO216 prote
44	366	18.4	421	21	AA588377	PRO216 (osteomodul
45	366	18.4	421	22	AAU12322	Human PRO216 polyp

ALIGNMENTS

```

RESULT 1
AA801311
ID AA801311 standard; Protein: 379 AA.
XX
AC AA801311;
XX
DT 25-SEP-2000 (first entry)
XX
DE Human PRO241 polypeptide.
XX
KW PRO; membrane bound protein; secreted protein; PRO357; PRO327;
KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO344; PRO347;
KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
KW antibody; screening; detection; inhibition; probe; primer; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT Modified-site /label= Signal peptide
FT Modified-site 129..135
FT Domain /note= "N-myristoylation site"
FT Modified-site 154..176
FT Modified-site /label= Leucine zipper pattern
FT Modified-site 210..216
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 214..220
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 214..220
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 237..243
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 270..276

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FT Modified-site /note= "N-myristoylation site"
 FT 281..285
 FT /note= "N-glycosylation site"
 FT Modified-site 282..288
 FT /note= "N-myristoylation site"
 XX
 XX WO200032776-A2.
 XX
 XX PN
 XX PD 08-JUN-2000.
 XX
 XX PF 01-DEC-1999; 99WO-US28301.
 XX
 XX PR 01-DEC-1998; 98WO-US25108.
 XX PR 16-DEC-1998; 98US-0112850.
 XX PR 22-DEC-1998; 98US-0113296.
 XX
 XX PA (GETH) GENENTECH INC.
 XX
 XX PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 XX PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 XX PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 XX WPI; 2000-412324/35.
 XX N-PSDB; AAA49551.
 XX
 XX PT New human nucleic acids encoding secreted and transmembrane
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 XX
 XX PS Claim 12; Fig 2; 187pp; English.
 XX
 XX CC New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources.
 XX
 XX SQ Sequence 379 AA;
 Query Match 100.08; Score 1992; DB 21; Length 379;
 Best Local Similarity 100.08; Pred. No. 4e-177;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKEYVLLFLALCSAKPFPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60
 DB 1 MKEYVLLFLALCSAKPFPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60
 61 PRSHFFPDLFPMCPGCGOCYSRVHCSDGLTSTVPTNIPFTRMLDLQNNKIKEIKEND 120
 61 PRSHFFPDLFPMCPGCGOCYSRVHCSDGLTSTVPTNIPFTRMLDLQNNKIKEIKEND 120
 QY 121 FKGLTSLYLILNNKLTTHPKAFITTKKRLRYLSHNSOLSEIPLNPKSLAEULRIHEN 180
 DB 121 FKGLTSLYLILNNKLTTHPKAFITTKKRLRYLSHNSOLSEIPLNPKSLAEULRIHEN 180
 QY 181 KVKIKQKDFKGMNALHVLMSANPLDNGIEPGAFEGVTVEFHIAEAKLTSPKGLPP 240
 DB 181 KVKIKQKDFKGMNALHVLMSANPLDNGIEPGAFEGVTVEFHIAEAKLTSPKGLPP 240
 QY 241 TLELHLDYNTKSTVELEDFKRYKELQRLGKNNKITDIENGSLANIPRVREIHLNKKL 300
 DB 241 TLELHLDYNTKSTVELEDFKRYKELQRLGKNNKITDIENGSLANIPRVREIHLNKKL 300
 QY 301 KKTPSGLPELKYLIQITFLHSNSTARVGVNDFCTVPKMKKSLYSALSFNNPKVWEMQP 360
 DB 301 KKTPSGLPELKYLIQITFLHSNSTARVGVNDFCTVPKMKKSLYSALSFNNPKVWEMQP 360
 QY 361 ATRFCVLSRMSVOLGNFGM 379
 DB 361 ATRFCVLSRMSVOLGNFGM 379

RESULT 2

AAU12335
 ID AAU12335 standard; Protein; 379 AA.
 XX
 XX AC AAU12335;
 XX
 XX DT 24-OCT-2001 (first entry)
 XX
 XX DE Human PRO241 polypeptide sequence.
 XX
 XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200140466-A2.
 XX
 XX PD 07-JUN-2001.
 XX
 XX PF 01-DEC-2000; 2000WO-US32678.
 XX
 XX PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 08-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 XX PA (GETH) GENENTECH INC.
 XX
 XX PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 XX WPI; 2001-408281/43.
 XX N-PSDB; AAS21407.
 XX
 XX PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 other PRO polypeptides, link bioactive molecules to cells expressing
 PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 XX PS Claim 12; Fig 328; 813pp; English.
 XX
 XX CC AAU2172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing

	CC hypertrophy, trauma, cancer, age-related macular degeneration,
	CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
	CC angina, myocardial infarctions, thromboembolitis, lymphangitis, tumour
	CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
	CC healing. The present sequence is a PRO protein of the invention.
XX	
SQ	Sequence 379 AA;
	Query Match 100.0%; Score 1992; DB 23; Length 379; Best Local Similarity 100.0%; Pred. No. 4e-177; Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY	121 FKGLTSLYGLILNNNKLTPIHKPAFLTTKKRLRYLSHNQLSEIPLNLPKSLAELRIHEN 180
Dy	121 FKGLTSLYGLILNNNKLTPIHKPAFLTTKKRLRYLSHNQLSEIPLNLPKSLAELRIHEN 180
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Dy	241 TLELHLDYNKISTVELEDFKRYKELOIGLGNNKITDIENGSIANTPRVRHEIHLENKL 300
OY	301 KITPSGPLPELKYLQIIIFLHSNSTARGVNDPCPTVMKKKSLSAISLNFNPVKYWEMQP 360
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OY	361 ATRCVLRSMVSVOLGNFGM 379
Dy	361 ATRCVLRSMVSVOLGNFGM 379
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ABB84831	ID ABB84831 standard; Protein; 379 AA. XX ABB84831;
DT	16-MAY-2002 (first entry)
DE	Human PRO241 protein sequence SEQ ID NO:30. KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; KW vulneray; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; KW gene therapy; cardiovascular disorder; endothelial disorder; cancer; KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; KW age-related macular degeneration; arterial stenosis; angina; KW rheumatoid arthritis; myocardial infarction; thromboembolitis; KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; KW wound healing; chromosome mapping; gene mapping. XX Homo sapiens. OS XN WO200200690-A2. XX XP 03-JAN-2002. XX XP 20-JUN-2001; 2001WO-US19692. XX PR 23-JUN-2000; 2000US-213637P. PR 20-JUL-2000; 2000US-219556P. PR 25-JUL-2000; 2000US-220624P. PR 25-JUL-2000; 2000US-220664P. PR 28-JUL-2000; 2000WO-US2071O. PR

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 Db 181 KVKIKQDTEFGKGMNALHVELEDEKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 240
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 Db 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSFLNNPVKYWEMQP 360
 361 ATFCVLSRMSVOLGNFGM 379
 361 ATFCVLSRMSVOLGNFGM 379

RESULT 5

AA017820

ID AAY17820 standard; Protein; 379 AA.

XX

AC AAY17820;

XX 12-AUG-1999 (first entry)

DT Human PRO241 protein sequence.

XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;

KW secreted protein; transmembrane protein; inflammation disorder.

XX OS Homo sapiens.

XX WO9928462-A2.

XX PD 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25108.

XX 25-FEB-1998; 98US-0075945.

XX 03-DEC-1997; 97US-0067411.

XX 11-DEC-1997; 97US-0069278.

XX 11-DEC-1997; 97US-0069334.

XX 11-DEC-1997; 97US-0069335.

XX 12-DEC-1997; 97US-0069425.

XX 16-DEC-1997; 97US-0069694.

XX 16-DEC-1997; 97US-0069696.

XX 16-DEC-1997; 97US-0069702.

XX 17-DEC-1997; 97US-0069870.

XX 17-DEC-1997; 97US-0069873.

XX 18-DEC-1997; 97US-0068017.

XX 05-JAN-1998; 98US-0070440.

XX 09-FEB-1998; 98US-0074086.

XX 09-FEB-1998; 98US-0074092.

XX (GETH) GENENTECH INC.

XX Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;

XX Yuan J;

XX WPI; 1999-371118/31.

XX N-PSDB; AAX80043.

XX Nucleic acids encoding PRO secreted and transmembrane proteins

XX Claim 12; Fig 2; 123pp; English.

XX The present invention describes nucleic acids encoding PRO secreted and

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CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.

SQ Sequence 379 AA;

Query Match 99.9%; Score 1990; DB 20; Length 379;

Best Local Similarity 99.7%; Pred. No. 6.2e-177;

Matches 378; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKEYVLLLFALCSAKPFPSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60

Db 1 MKEYVLLLFALCSAKPFPSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTR 60

Qy 61 PRSHFFPDLFPMCPFGCOCYSRVVHCSDGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120

Db 61 PRSHFFPDLFPMCPFGCOCYSRVVHCSDGLTSVPTNIPDTRMLDLQNNKIKEIKEND 120

Qy 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 180

Db 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 180

Qy 181 KVKIKQDTEFGKGMNALHVELEDEKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 240

Db 181 KVKIKQDTEFGKGMNALHVELEDEKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 240

Qy 241 TLELHLDYNNKISTVELEDEKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 300

Db 241 TLELHLDYNNKISTVELEDEKRYKELQRLGLGNKTTDIENGSLANIPRVREIHLNNKL 300

Qy 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSFLNNPVKYWEMQP 360

Db 301 KKIPSGLPKYLQIIFLHNSIARVGVNDFCPTVPKMKKSLYSALSFLNNPVKYWEMQP 360

Qy 361 ATFCVLSRMSVOLGNFGM 379

Db 361 ATFCVLSRMSVOLGNFGM 379

RESULT 6

AAE05347

ID AAE05347 standard; Protein; 373 AA.

XX

AC AAE05347;

XX 12-SEP-2001 (first entry)

DT Mouse bone/cartilage proteoglycan I (BGN) protein.

XX Mouse; cytostatic; antinflammatory; immunoregulatory; tissue integrity;

KW wound healing; immune response; vaccine; cancer; asthma; allergy;

KW cell trafficking; BGN; bone/cartilage proteoglycan I protein;

KW biglycan; PG-S1; secreted protein; therapy.

XX Mus sp.

XX WO200148192-A1.

XX 05-JUL-2001.

XX 21-DEC-2000; 2000WO-NZ00256.

XX 23-DEC-1999; 99US-0171678.

XX 28-NOV-2000; 2000US-0724864.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Murison JG;

XX

WPI: 2001-425665/45.
N-PSDB: AAD10114.

Novel isolated polypeptide useful to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target

Claim 6: Page 76-77; 101pp; English.

The patent discloses novel polynucleotides and their corresponding proteins which play a major role in induction of growth, cell migration and proliferation, cell-cell interaction and the differentiation of tissue-specific cells. These proteins are important in the maintenance of tissue integrity and thus are important in wound healing. They are useful in various assays to determine the biological activity, to raise antibodies, to isolate corresponding interacting proteins or other compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target in a whole range of disease states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynucleotides of the invention are useful in genome and physical mapping, in positional cloning of genes, to tag or identify an organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response as part of a vaccine or anti-cancer treatment, as target for cancer treatment, as immunoregulatory and anti-inflammatory molecule, as diagnostic for specific types of cancer and for development of an anti-cancer treatment, and as a target for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit or enhance the activity of the soluble molecule that binds proteins of the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant. The present sequence is bone/cartilage proteoglycan I (BGN) protein, a secreted protein from mouse. BGN is also known as biglycan or PG-S1.

Sequence 373 AA:

Query Match 90.3%; Score 1799; DB 22: Length 373;

Best Local Similarity 90.2%; Pred. No. 3.9e-159;

Matches 341; Conservative 17; Mismatches 14; Indels 6; Gaps 1;

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115 FGKLSLYALILNKKLTTHPKFTFTTKKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 174
QY 181 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHIRAEAKLTSVPKGLPP 240
DB 175 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHIRAEAKLTSVPKGLPP 234
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DB 235 TLELHLDYNKISTVELEDFKRYELQRLGLGNKTTDIEGSLANIPRVREIHLNKKL 294
QY 301 KIPSGLPKLYLOITFLHNSIARVGVNDFTVPMKSKSYLSAISLNNPKYVEMOP 360
DB 295 KIPSGLPKLYLOITFLHNSIARVGVNDFTVPMKSKSYLSAISLNNPKYVEMOP 354
QY 361 ATRCVLSRMSVOLGNFG 378
DB 355 ATRCVLSRMSVOLGNVG 372

RESULT 7
ABB72356

ABB72356 standard; Protein; 373 AA.

ABB72356;

04-APR-2002 (first entry)

Murine protein isolated from skin cells SEQ ID NO: 680.

Human; rat; mouse; skin cell; skin wound; cancer; growth defect;

developmental defect; inflammatory disease; dermatological; vulnary;

immunomodulator; anti-inflammatory; cytostatic; neuroprotective.

Mus sp.

WO200190357-A1.

29-NOV-2001.

24-MAY-2001; 2001WO-NZ000099.

24-MAY-2000; 2000US-206650P.

25-JUL-2000; 2000US-22132P.

(GENE-) GENESIS RES & DEV CORP LTD.

Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;

WPI: 2002-122020/16.

N-PSDB: ABL35045.

New polynucleotides and polypeptides encoded by the polynucleotides

isolated from skin cells, useful for treating skin wounds, cancers,

growth and developmental defects, inflammatory diseases, or for

modulating immune responses

Claim 4; Page 434-435; 466pp; English.

The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.

Sequence 373 AA:

Query Match 90.3%; Score 1799; DB 23: Length 373;

Best Local Similarity 90.2%; Pred. No. 3.9e-159;

Matches 341; Conservative 17; Mismatches 14; Indels 6; Gaps 1;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDNSLFPPTRE 60
DB 1 MKEYVLLLLAVCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDNSLFPPTRE 54
QY 61 PRSHFFPDLFPMCPFCGQCYSRVVHCSDLGLTSVPTNIPFDTMRDLQNNKIKEIKEND 120
DB 55 PVNPFPPDLFPMCPFCGQCYSRVVHCSDLGLTSVPTNIPFDTMRDLQNNKIKEIKEND 114
QY 121 FGKLSLYGLILNKKLTTHPKAFITTKKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 180
DB 115 FGKLSLYALILNKKLTTHPKFTFTTKKRLRLYLSHNQLSEIPLNPKSLAEIRIHEN 174
QY 181 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHIRAEAKLTSVPKGLPP 240
DB 175 KVKIKQDFTKGMNALHVLMSANPLDNGIEPGAFEGVTVFHIRAEAKLTSVPKGLPP 234
QY 241 TLELHLDYNKISTVELEDFKRYELQRLGLGNKTTDIEGSLANIPRVREIHLNKKL 300
DB 235 TLELHLDYNKISTVELEDFKRYELQRLGLGNKTTDIEGSLANIPRVREIHLNKKL 294

QY 301 KIPSGLPKYLQIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSLFNNPVKYMWP 360
 DB 295 KIPSGLOELKYLQIIFLHNSIAKGVNDPCPTVPKMKKSLYSALSLFNNPKYWEIQP 354
 QY 361 ATRFVLSRMSVQLGNFG 378
 DB 355 ATRFVLSRMSVQLGNVG 372

RESULT 8

AA040351 ID AAM40351 standard; Protein: 344 AA.

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

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XX AAM40351;

XX AAM40351;

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XX AAM40351;

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XX AAM40351;

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XX AAM40351;

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XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX AAM40351;

XX SQ

Sequence 344 AA;

Query Match

Best Local Similarity 82.8%; Score 1649; DB 22; Length 344;

Matches 316; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 56 FPTREPRSHFFDLPMPGFCQCYSRVHCSDLGLTSVPTNIPEDTRMLDQNNKIKE 115

DB 21 FOESQEAIFFPDLPMPGFCQCYSRVHCSDLGLTSVPTNIPEDTRMLDQNNKIKE 80

QY 116 IKENDEKGLTSLYGLILNNKLTTHPKAFLTKKLRRLYLSHNSLSEPLNPKSLAEL 175

DB 81 IKENDEKGLTSLYGLILNNKLTTHPKAFLTKKLRRLYLSHNSLSEPLNPKSLAEL 140

QY 176 RIHENVKVKIQDKTFKGMNHLVLEMSANPLDNGNIEGAFEGVTVFHIRIAEAKLTSVP 235

DB 141 RIHENVKVKIQDKTFKGMNHLVLEMSANPLDNGNIEGAFEGVTVFHIRIAEAKLTSVP 200

QY 236 KGLPPTLLEHLHDYNNKISTVELEDEKRYKELQRLGLGNNKITDIEGSLANIPRVREIHL 295

DB 201 KGLPPTLLEHLHDYNNKISTVELEDEKRYKELQRLGLGNNKITDIEGSLANIPRVREIHL 260

QY 296 ENNKKKIPSGLPKYLQIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSLFNNPVKY 355

DB 261 ENNKKKIPSGLPKYLQIIFLHNSIARVGVNDPCPTVPKMKKSLYSALSLFNNPVKY 320

QY 356 WEMQPATFRCVLSRMSVQLGNFGM 379

DB 321 WEMQPATFRCVLSRMSVQLGNFGM 344

RESULT 9

ABG22569 ID ABG22569 standard; Protein: 352 AA.

XX AC ABG22569;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #22560.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PW WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS86756.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity

XX PS Claim 20; SEQ ID No 52928; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC specification.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

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CC specification.

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CC specification.

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CC specification.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 352 AA;

Query Match 78.2%; Score 1558; DB 22; Length 352;
 Best Local Similarity 93.6%; Pred. No. 1.1e-136;
 Matches 305; Conservative 3; Mismatches 16; Indels 2; Gaps 2;
 QY 56 FPTREPRSHFFPDLFPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKE 115
 DB 27 FOESQEAIFPFDLPFCMPFCQCYSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKE 86
 QY 116 IKENDFKGLTSYGLILNNKLTTHPKAFLTTRKRLRYLSHNSLSEIPLNPKSLAEL 175
 DB 87 IKENDFKGLTSYGLILNNKLTTHPKAFLTTRKRLRYLSHNSLSEIPLNPKSLAEL 146
 QY 176 RIHENVKVKIQDKTFKGMNALHVLMSANPLDNN-GIEPGAF-EGVTVFHRIAEAKLTS 233
 DB 147 RIHENVKVKIQDKTFKGMNALHVLMSANPLXXSWGIEPGAFXRCXSYTRIAEAKLTS 206
 QY 234 VPKGLPPTLLEHLHDYKNKISTVELEDFRYKELORGLGNKNTIDENGSLANIPRVREI 293
 DB 207 VPKGLPPTLLEHLHDYKNKISTVELEDFRYKELORGLGNKNTIDENGSLANIPRVREI 266
 QY 294 HLENKWLKIPSGLPKLYLQIFLHNSIARVGVNDPCPTVPMKKSLSYSAISLFFNNPV 353
 DB 267 HLGNIKKIPSGLPKLYLQIFLHNSIARVGVNDPCPTVPMKKSLSYSAISLFFNNPV 326
 QY 354 KYWEMQPATFRCVLSRMSVOLGNFGM 379
 DB 327 KYWEMQPATFRCVLSRMSVOLGNFGM 352

RESULT 10

95678

AA895678 standard; Protein; 246 AA.

XX AA895678;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:18473.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX (HELL-) HELIX RES INST.
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 DR
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 18473; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB98893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

SQ Sequence 246 AA;

Query Match 62.1%; Score 1237; DB 22; Length 246;

Best Local Similarity 96.7%; Pred. No. 5.4e-107;

Matches 237; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDT-----DDDDDDDDDDDDDDNSLF 56

DB 1 MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDDDNSLF 60

QY 57 PTERPSRSHFFPDLFPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEI 116

DB 61 PTERPSRSHFFPDLFPMCPFCQCYSRVVHCSDLGLTSVPTNIPFDTMLDLQNNKIKEI 120

QY 117 KENDFKGLTSYGLILNNKLTTHPKAFLTTRKRLRYLSHNSLSEIPLNPKSLAELR 176

DB 121 KENDFKGLTSYGLILNNKLTTHPKAFLTTRKRLRYLSHNSLSEIPLNPKSLAELR 180

QY 177 IHENKVKIKQDKTFKGMNALHVLMSANPLDNNNGIEGAFEGVTVFHRIAEAKLTSVPK 236

DB 181 IHENKVKIKQDKTFKGMNALHVLMSANPLDNNNGIEGAFEGVTVFHRIAEAKLTSVPK 240

QY 237 GLPPT 241

DB 241 DNLFS 245

RESULT 11

AA887951

ID AA887951 standard; Protein; 369 AA.

XX AA887951;

XX AC AA887951;

XX XX

DT 20-MAR-1996 (first entry)
 XX Rat neurotrophic biglycan.
 DE Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
 XX neurotrophic; central nervous system; CNS; memory loss; dementia;
 KW learning.
 KW
 XX Rattus sp.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..37
 FT Region /label= Sig_peptide
 FT 44..60
 FT /label= Hypervariable_region
 XX WO9530432-A1.
 XX 16-NOV-1995.
 XX 09-MAY-1994; 94WO-EP01479.
 XX 09-MAY-1994; 94WO-EP01479.
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX Hasenoechl R, Huston J, Junghans U, Kappler J, Koops A;
 PI Mueller HW;
 XX WPI; 1995-403938/51.
 DR N-PSDB; AAT08768.
 DR
 XX Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s)
 PT for maintain structural and function of the CNS and attenuating
 PT memory deficit(s) in the elderly and patients with dementia
 XX
 PS Claim 1; Page 44-45; 60pp; English.
 XX Rat biglycan (AAB87951) is a chondroitin sulphate proteoglycan with
 CC neurotrophic activity for brain neurons. Recombinant biglycan,
 CC obt'd. by expression of encoding cDNA (AAT08768) in eukaryotic host
 CC cells, can be used to enhance the survival and maintain the structure
 CC and function of CNS neurons during normal aging as well as after
 CC pathological and/or traumatic nervous system damage. It can also
 CC be used to restore function following nervous system lesions and
 CC degenerative diseases, and to improve learning efficiency and memory
 CC in the elderly and in patients with dementia.
 XX
 PS Sequence 369 AA;
 XX
 Query Match 52.2%; Score 1040.5; DB 16; Length 369;
 Best Local Similarity 52.6%; Pred. No. 2e-88;
 Matches 199; Conservative 67; Mismatches 93; Indels 19; Gaps 3;
 QY 4 YVLLFLALCSAKPF-----FSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLPFTR 59
 DB 5 WLLTLLALLSQALPEQKGFWDFTLDDGLLMMNDEERASGDTTSGVPDL-----SLTPT- 59
 QY 60 EPRSHFFPDLFPMCPGCGOCYSRVVHCSDLGLTSVPTNIPFFRMLDLQNNKIKEKEN 119
 DB 60 -----FSAMCPGCHLRVQCSDLGLTKVPEKISPTDTLLDLQNNDISLRKD 109
 QY 120 DFKGTSYGLILNNKLTIKHPKAFITTKRLRLYLHSHNOLSPILNLPKSLAELRIHE 179
 DB 110 DFKGLHLYALVNVNKSISKIHEKAFSPRLKQKLYISKNHVLPNLPSSLVLEIRIHD 169
 QY 180 NKVKIKQDTFGKGNALHVLMSANPLDNGIEPAGFEGVTVFHRIAEAKLTSPVKGLP 239
 DB 170 NRIKVPKGVFSGLRNMCIEMGNPLNENSGFEPGADGLKLVLRISAKLTGIPKLP 229
 QY 240 PTLLEHLHDYKISTVELEDFKRYKELQRLGLGNKTTDIENGSLANIIPVREIHLENNK 299
 DB 230 ETLNELHLDHNNKIQAIIELEDLRLSKYLRUGLGHQIRMIENGSLSLFPLTLRELHLDNNK 289

QY 300 LKIPSGLPKLYQLIIFLHNSIARVGVNDFQPTVPKMKKSLYSALSLENNPKYWEHQ 359
 DB 290 LSRVAGLPDLKLQVYVYLLHNSNITKVGINDFCPMGFGVKRAYYIGISLFNPNVPYWEVO 349
 QY 360 PATFRCLVSRMSVOLGNF 377
 DB 350 PATFRCVTDRLATQFGNY 367
 RESULT 12
 AAB85043
 ID AAB85043 standard; Protein; 368 AA.
 XX
 AC AAB85043;
 XX
 DT 06-AUG-2001 (first entry)
 XX Human biglycan protein sequence.
 DE
 XX
 KW Dystrophin-associated protein complex; DAPC; postsynaptic membrane;
 KW biglycan; muscular dystrophy; neuromuscular; neurological; smooth muscle;
 KW nontropic; neuroleptic; antiviral.
 XX
 OS Homo sapiens.
 XX
 PN WO200136475-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-US31661.
 XX
 PR 18-NOV-1999; 99US-0166253.
 XX
 PA (UYBR-) UNIV BROWN RES FOUND.
 XX
 PI Fallon J, McKechnie B, Rafii M, Creely H, Bowe M, Ferri R;
 WPI: 2001-355617/37.
 DR N-PSDB; AAF83977.
 XX
 PT Stabilizing dystrophin-associated protein complexes and activating
 PT postsynaptic membrane of a cell for treating or preventing muscular,
 PT neuromuscular and neurological disorders, involves contacting cell with
 PT biglycan
 XX
 PS Disclosure: Page 101-108; 112pp; English.
 XX
 CC The invention relates to stabilizing dystrophin-associated protein
 CC complexes (DAPCs) on the surface of a cell or activating a postsynaptic
 CC membrane of a cell that comprises contacting the cell with an effective
 CC amount of biglycan. A composition comprising biglycan or its portion
 CC is useful for treating or preventing a condition associated with abnormal
 CC DAPC in cells, characterized by breakdown of muscle cell membrane, which
 CC includes muscular dystrophies, such as Duchenne's, Becker's, Congenital,
 CC Limb-girdle muscular dystrophy and myotonic dystrophy and a condition
 CC characterized by abnormal neuromuscular junction or synapse, such as
 CC neuromuscular or neurological diseases in a subject. Neurological
 CC disorders, include polymyositis and Alzheimer's disease. Biglycan is also
 CC useful for preventing and treating smooth muscle disorders, such as
 CC cardiac myopathies and for treating and inhibiting infections of cells by
 CC microorganisms e.g. viruses. Agents that modulate the activity of
 CC DAG-125, identified by the methods are useful in the prophylactic and
 CC therapeutic treatments of diseases or disorders, characterized by an
 CC unstable DAPC or an inappropriate formation of a postsynaptic
 CC differentiation. Biglycans are also useful as a supplement to brain or
 CC muscle cell or tissue culture and, tissues can be incubated in vitro
 CC with biglycan to reverse tissue atrophy and to improve their growth or
 CC survival in vitro. The present sequence represents the human biglycan.
 XX
 SQ Sequence 368 AA;
 Query Match 51.9%; Score 1034; DB 22; Length 368;

Claim 3; Fig 8; 60pp; English.

Human biglycan (AAR87952) is a chondroitin sulphate proteoglycan with neurotrophic activity for brain neurons. It can be used to enhance the survival and maintain the structure and function of CNS neurons during normal ageing as well as after pathological and/or traumatic nervous system damage. It can also be used to restore function following nervous system lesions and degenerative diseases, and to improve learning efficiency and memory in the elderly and in patients with dementia.

XX
SQ Sequence 369 AA;

Query Match 51.8%; Score 1031.5; DB 16; Length 369;
Best Local Similarity 52.9%; Pred. No. 1.4e-87;
Matches 199; Conservative 64; Mismatches 94; Indels 19; Gaps

QY 6 LLLFLALCSAKPF----FSPSHIALKNMKDKMEDTDDDDDDDDDDDDDDNSLFTPTREP 61
DB 7 LVSLALLSQALPFQGRGFNDFTLDDGPFWMNDEASGADTTSGVLDPD---SVTPYS- 61

QY 62 RSHFFPDLPMCFPGGOCYRVVHCSDLGLTSTVPTNIPFDTRMLDLQNNKIKEIENDF 121
DB 62 -----AMCPFGCHCLRYYQCSDLGLSKVPKEISPTFTLLDQLQNNDISERKDDF 111

QY 122 KGLTSLGLIILNNKLFTHPKAFLTTKKLRLRLYLISHNQISEIPLNLPKSLAELRTHENK 181
DB 112 KGLQHLVALVLNNKISKIHEKAFSLPKLQKLYISKNHLVEIPNLPSSLVELRLIHDNR 171

QY 182 VKKIQKDTFKGMNALHVLMSANPLDNNIGEPGAEVGVTVFHIRTAEAKLTSVPKGLPPT 241
DB 172 IRKVPKGVFSGLRNNCIEGMGNPLENSGFEFGDGLKLYLRISAEKLRGIPKDLPET 231

QY 242 LLELHLDYKNKISTVEDEFKRYEKLORLGLGNKKTIDIEGSLANIPRVRIHLENNK 301
DB 232 LNELHLDHDKHQATELEDLLRYSKLRLGLGHNQIRMIENGSLSELPTRLRELHLDNNKLS 291

QY 302 KIPSGLPEIKYLQILFIHLSNLSIARGVYNDFCPTVPKMKKLSYSAISLNNPVKTWEQPA 361
DB 292 RVPAGLPDLKLLQVYVYLLHSNNITKGVYNDFCPMGFGVKRAYTNGISLFNNPVYWEVQPA 351

QY 362 TPRCVLSRMSVQLGNF 377
DB 352 TPRCVTDRLATQFGNY 367

RESULT 14
AAG78510
ID AAG78510 standard; protein; 368 AA.
XX
AC AAG78510;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human biglycan amino acid sequence.
XX
KW Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix;
KW TGF-beta; Transforming growth factor-beta; Burn; Wound; Cytostatic;
KW Nephrotropic; Antirheumatic; Antiarthritis; Vasotropic; Vulnerary
KW Antiartherosclerotic; Hepatotropic; Cardiant; Dermatological;
KW Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis;
KW Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.
XX
OS Homo sapiens.
XX
PN USG277812-B1.
XX
PD 21-AUG-2001.
XX
PF 02-JUN-1995; 95US-0458834.
XX
PR 14-NOV-1991; 91US-0792192.
PR 17-NOV-1992; 92US-0978931.

[illegible]

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 16:04:11 ; Search time 23 Seconds
(without alignments)
1634.193 Million cell updates/sec

Title: US-09-944-457-2

Perfect score: 1992

Sequence: 1 MREYVLLFLALCSAKPFES.....PATFRCVLSRMSVOLGNFGM 379

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1992	100.0	379	9	US-09-944-413-2
2	1992	100.0	379	9	US-09-944-403-2
3	1992	100.0	379	9	US-09-944-896-2
4	1992	100.0	379	9	US-09-944-944-2
5	1992	100.0	379	9	US-09-944-907-2
6	1992	100.0	379	9	US-09-944-929-2
7	1992	100.0	379	9	US-10-028-072-328
8	1992	100.0	379	9	US-10-121-049-328
9	1992	100.0	379	9	US-10-123-904-328
10	1992	100.0	379	9	US-10-140-470-328
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27	1992	100.0	379	9	US-10-123-261-328
28	1992	100.0	379	9	US-10-140-921-328
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32	1992	100.0	379	9	US-10-123-903-328
33	1992	100.0	379	9	US-10-124-819-328
34	1992	100.0	379	9	US-10-124-822-328
35	1992	100.0	379	9	US-10-140-925-328
36	1992	100.0	379	9	US-10-160-498-328
37	1992	100.0	379	9	US-09-944-884-2
38	1992	100.0	379	9	US-10-121-041-328
39	1992	100.0	379	9	US-10-121-043-328
40	1992	100.0	379	9	US-10-121-047-328
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44	1992	100.0	379	9	US-10-123-909-328
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ALIGNMENTS

RESULT 1

US-09-944-413-2
; Sequence 2, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944.413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,596
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997


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: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020165143A1e1mb
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020165143A1e1mb
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 2
: LENGTH: 379
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-09-944-403-2

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	Matches 379; Conservative	0;	Mismatches	0;	Indels	0; Gaps
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Db	181	KYKKTKQDTFGMNAHVLMSANPLDNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPP	240
QY	241	TLELHLDYNNKISTVELEDEKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNNKL	300
Db	241	TLELHLDYNNKISTVELEDEKRYKELQRLGLGNKKTIDENGSLANIPRVREIHLNNKL	300
QY	301	KKIPSGLPKLYKIIFLHNSIARGVNDPCTVPKMKKSLYSALSIFNPNPKYKWMQP	360
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QY	361	ATFCVLSRMSVOLGNFGM	379
Db	361	ATFCVLSRMSVOLGNFGM	379
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US-09-944-896-2			
: Sequence 2, Application US/09944896			
: Patent No. US20020168715A1			
: GENERAL INFORMATION:			
: APPLICANT: Baker, Kevin			
: APPLICANT: Botstein, David			
: APPLICANT: Eaton, Dan			
: APPLICANT: Ferrara, Napoleone			
: APPLICANT: Filvaroff, Ellen			
: APPLICANT: Gerritsen, Mary			
: APPLICANT: Goddard, Audrey			
: APPLICANT: Godowski, Paul			
: APPLICANT: Grimaldi, Christopher			
: APPLICANT: Gurney, Austin			
: APPLICANT: Hillan, Kenneth			
: APPLICANT: Kljavin, Ivar			
: APPLICANT: Napier, Mary			
: APPLICANT: Roy, Margaret			
: APPLICANT: Tumas, Daniel			
: APPLICANT: Wood, William			
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
: FILE NO OF INVENTION: ACIDS ENCODING THE SAME			
: FILE REFERENCE: P2548P1C1			
: CURRENT APPLICATION NUMBER: US/09/944,896			
: CURRENT FILING DATE: 2001-08-31			
: PRIOR APPLICATION NUMBER: 09/866,028			
: PRIOR FILING DATE: 2001-05-25			
: PRIOR APPLICATION NUMBER: 60/069,334			
: PRIOR FILING DATE: December 11, 1997			
: PRIOR APPLICATION NUMBER: 60/069335			
: PRIOR FILING DATE: December 11, 1997			
: PRIOR APPLICATION NUMBER: 60/069,278			
: PRIOR FILING DATE: December 11, 1997			
: PRIOR APPLICATION NUMBER: 60/069,425			
: PRIOR FILING DATE: December 12, 1997			
: PRIOR APPLICATION NUMBER: 60/069,696			
: PRIOR FILING DATE: December 16, 1997			
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: PRIOR FILING DATE: December 16, 1997			
: PRIOR APPLICATION NUMBER: 60/069,702			
: PRIOR FILING DATE: December 16, 1997			
: PRIOR APPLICATION NUMBER: 60/069,870			
: PRIOR FILING DATE: December 17, 1997			
: PRIOR APPLICATION NUMBER: 60/069,873			
: PRIOR FILING DATE: December 17, 1997			
: PRIOR APPLICATION NUMBER: 60/068,017			
: PRIOR FILING DATE: December 18, 1997			
: PRIOR APPLICATION NUMBER: 60/070,440			
: PRIOR FILING DATE: January 5, 1998			

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QY 361 ATRCVLSRMSVOLGNFGM 379

Db 361 ATRCVLSRMSVOLGNFGM 379

RESULT 6

US-09-944-929-2

; Sequence 2, Application US/09944929

; Publication No. US20020197612A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944, 929

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866, 028

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 2

; LENGTH: 379

; TYPE: PRT

; ORGANISM: Homo Sapien

US-09-944-929-2

Query Match 100.0%; Score 1992; DB 9; Length 379;

Best Local Similarity 100.0%; Pred. No. 8.6e-159;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 PRSHFFPDLFPMCPGQCQYRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKETKEND 120

QY 121 FKGLTSYGLILNNKTKTHPKAFLTTKKLRRLYLHNSQLSDIPLNPKSLAELRIHEN 180

Db 121 FKGLTSYGLILNNKTKTHPKAFLTTKKLRRLYLHNSQLSDIPLNPKSLAELRIHEN 180

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Db 181 KVKKIQDTPFGMALHVLMSANPLDNNGIEPCAGVTVFHRTAEAKLTSVPKGLPP 240

QY 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANIPRVREIHLNNKL 300

Db 241 TLELHLDYNNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANIPRVREIHLNNKL 300

QY 301 KKIPLGPELKYLIIFLHNSIARVGVNDFCPVPMKMSLYSALSIFLNNPVKYWQ 360

Db 301 KKIPLGPELKYLIIFLHNSIARVGVNDFCPVPMKMSLYSALSIFLNNPVKYWQ 360

QY 361 ATRCVLSRMSVOLGNFGM 379

Db 361 ATRCVLSRMSVOLGNFGM 379

RESULT 7

US-10-028-072-328

; Sequence 328, Application US/10028072

; Publication No. US20030004311A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang

; TITLE OF INVENTION:

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/028, 072

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

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; PRIOR APPLICATION NUMBER: 60/059836

; PRIOR FILING DATE: 1997-09-24

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/062285

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; PRIOR APPLICATION NUMBER: 60/062287

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; PRIOR APPLICATION NUMBER: 60/063127

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063327

; PRIOR FILING DATE: 1997-10-27

; PRIOR APPLICATION NUMBER: 60/063329

; PRIOR FILING DATE: 1997-10-27

; PRIOR APPLICATION NUMBER: 60/063550

; PRIOR FILING DATE: 1997-10-28

1	PRIOR FILING DATE: 1998-05-07	
2	PRIOR APPLICATION NUMBER: 60/084627	
3	PRIOR FILING DATE: 1998-05-07	
4	PRIOR APPLICATION NUMBER: 60/084637	
5	PRIOR FILING DATE: 1998-05-07	
6	PRIOR APPLICATION NUMBER: 60/085149	
7	PRIOR FILING DATE: 1998-05-12	
8	PRIOR APPLICATION NUMBER: 60/085323	
9	PRIOR FILING DATE: 1998-05-13	
10	PRIOR APPLICATION NUMBER: 60/085338	
11	PRIOR FILING DATE: 1998-05-13	
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17	PRIOR FILING DATE: 1998-05-15	
18	PRIOR APPLICATION NUMBER: 60/085704	
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21	PRIOR FILING DATE: 1998-05-22	
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23	PRIOR FILING DATE: 1998-05-22	
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25	PRIOR FILING DATE: 1998-05-28	
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27	PRIOR FILING DATE: 1998-06-04	
28	PRIOR APPLICATION NUMBER: 60/088730	
29	PRIOR FILING DATE: 1998-06-10	
30	PRIOR APPLICATION NUMBER: 60/088741	
31	PRIOR FILING DATE: 1998-06-10	
32	PRIOR APPLICATION NUMBER: 60/088810	
33	PRIOR FILING DATE: 1998-06-10	
34	PRIOR APPLICATION NUMBER: 60/088858	
35	PRIOR FILING DATE: 19/98-06-11	
36	PRIOR APPLICATION NUMBER: 60/089532	
37	PRIOR FILING DATE: 1998-06-17	
38	PRIOR APPLICATION NUMBER: 60/089599	
39	PRIOR FILING DATE: 1998-06-17	
40	PRIOR APPLICATION NUMBER: 60/089907	
41	PRIOR FILING DATE: 1998-06-18	
42	PRIOR APPLICATION NUMBER: 60/089947	
43	PRIOR FILING DATE: 1998-06-19	
44	PRIOR APPLICATION NUMBER: 60/090349	
45	PRIOR FILING DATE: 1998-06-23	
46	PRIOR APPLICATION NUMBER: 60/090429	
47	PRIOR FILING DATE: 1998-06-24	
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49	PRIOR FILING DATE: 1998-06-24	
50	PRIOR APPLICATION NUMBER: 60/090538	
51	PRIOR FILING DATE: 1998-06-24	
52	PRIOR APPLICATION NUMBER: 60/090863	
53	PRIOR FILING DATE: 1998-06-26	
54	PRIOR APPLICATION NUMBER: 60/091360	
55	PRIOR FILING DATE: 1998-07-01	
56	PRIOR APPLICATION NUMBER: 60/091519	
57	PRIOR FILING DATE: 1998-07-02	
58	PRIOR APPLICATION NUMBER: 60/091982	
59	PRIOR FILING DATE: 1998-07-02	

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Best Local Similarity 100.0%; Pred. No. 8.6e-159;
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Db 181 KVKIKQDFTFGMNAHLVLEMSANPLDNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
Qy 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNENKL 300
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; Sequence 328, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC17
; CURRENT APPLICATION NUMBER: US/10/121.049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 328
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-328

Query Match 100.0%; Score 1992; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 8.6e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60
Qy 61 PRSHFFPDLFPMCPFGCQCYSRVHCSDLGLTSVPTNIPFDTMRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFPDLFPMCPFGCQCYSRVHCSDLGLTSVPTNIPFDTMRMLDLQNNKIKEIKEND 120
Qy 121 FKGLTSLYGLILNNNKLTTHPKAFLLTKLRLRYLSHNLSEIPLNPKSLAEALRIHEN 180
Db 121 FKGLTSLYGLILNNNKLTTHPKAFLLTKLRLRYLSHNLSEIPLNPKSLAEALRIHEN 180
Qy 181 KVKIKQDFTFGMNAHLVLEMSANPLDNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
Db 181 KVKIKQDFTFGMNAHLVLEMSANPLDNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
Qy 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNENKL 300
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Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNENKL 300
Qy 301 KIPSGLPKLYQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSFLFNNPVKYWEMQP 360
Db 301 KIPSGLPKLYQIIFLHNSIARVGNDFCPTVPKMKKSLYSALSFLFNNPVKYWEMQP 360
Qy 361 ATFCVLSRMSVOLGNFGM 379
Db 361 ATFCVLSRMSVOLGNFGM 379

RESULT 9
US-10-123-904-328
; Sequence 328, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC54
; CURRENT APPLICATION NUMBER: US/10/123.904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 328
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-328

Query Match 100.0%; Score 1992; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 8.6e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60
Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPPTRE 60
Qy 61 PRSHFFPDLFPMCPFGCQCYSRVHCSDLGLTSVPTNIPFDTMRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFPDLFPMCPFGCQCYSRVHCSDLGLTSVPTNIPFDTMRMLDLQNNKIKEIKEND 120
Qy 121 FKGLTSLYGLILNNNKLTTHPKAFLLTKLRLRYLSHNLSEIPLNPKSLAEALRIHEN 180
Db 121 FKGLTSLYGLILNNNKLTTHPKAFLLTKLRLRYLSHNLSEIPLNPKSLAEALRIHEN 180
Qy 181 KVKIKQDFTFGMNAHLVLEMSANPLDNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
Db 181 KVKIKQDFTFGMNAHLVLEMSANPLDNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPP 240
Qy 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNENKL 300
Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKNTIDIEGSLANIPRVREIHLNENKL 300
```


Qy	301	KKISGPEUKYQIIFLHNSIARVGVNDCTVPKMKKSLYSATSLFNPNVKYWMQP	360
Db	301	KKISGPEUKYQIIFLHNSIARVGVNDCTVPKMKKSLYSATSLFNPNVKYWMQP	360
Qy	361	ATFCVLRSMSVOLGNFGM	379
Db	361	ATFCVLRSMSVOLGNFGM	379

RESULT 10
US-10-140-470-328
; Sequence 328, Application US/10140470
; Publication No. US20030022331A1

```

: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED A
: FILE REFERENCE: P330R1C160
: CURRENT APPLICATION NUMBER: US
: CURRENT FILING DATE: 2002-05-
: Prior Application removed - See
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 328
: LENGTH: 379
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-140-470-328

```

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Query Match          100.0%; Score 1992: DB 9; Length 379;
Test Local Similarity 100.0%; Pred. No. 8.6e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	MKEYVLLLFALCSAKPFFSPSHIALKNMMLKMDETDDDDDDDDDDDDDDDDDDNSLPFTRE	60
Dd	1	MKEYVLLLFALCSAKPFFSPSHIALKNMMLKMDETDDDDDDDDDDDDDDDDDDNSLPFTRE	60
Qy	61	PRSHFFPDLPMPCFQCQYSRVVHCSOLGITSVPTNIPEDTRMLDQNKKIKEIKEND	120
Dd	61	PRSHFFPDLPMPCFQCQYSRVVHCSOLGITSVPTNIPEDTRMLDQNKKIKEIKEND	120
Qy	121	FKGUTSGLYLNNNKLTUKTHPKAFITTKKLRRLYLSHNQLSEIPLNPKSLAELRIHEN	180
Dd	121	FKGUTSGLYLNNNKLTUKTHPKAFITTKKLRRLYLSHNQLSEIPLNPKSLAELRIHEN	180
Qy	181	KVKKIQKDTEFGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGCLPP	240
Dd	181	KVKKIQKDTEFGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGCLPP	240
Qy	241	TLLHLHDYNYKISTVELEDFKRYKELORLGNNKITDIENGLSANIPRYREIHLENKKL	300
Dd	241	TLLHLHDYNYKISTVELEDFKRYKELORLGNNKITDIENGLSANIPRYREIHLENKKL	300
Qy	301	KKIPSGLPULKYLIQILFLHSNSTARGVNDECPTVPKMKSLSYSAISLFNNPVKYWEMOP	360
Dd	301	KKIPSGLPULKYLIQILFLHSNSTARGVNDECPTVPKMKSLSYSAISLFNNPVKYWEMOP	360

QY 361 ATFRCLSRMSVOLGNFGM 379
 |||||
 Db 361 ATFRCLSRMSVOLGNFGM 379

RESULT 11.

US-10-175-746-328
; Sequence 328, Application US/10175746
; Publication No. US20030027270A1

```

: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330RIC353
: CURRENT APPLICATION NUMBER: US/10/175,746
: CURRENT FILING DATE: 2002-06-19
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 328
: LENGTH: 379
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-10-175-746-328

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Query Match	100.0%;	Score 1992;	DB 9;	Length 379;
Best Local Similarity	100.0%;	Pred. No. 8.6e-159;		
Matches 379;	Conservative 0;	Mismatches 0;	Indels 0	

Qy	1	MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDSDNLSLFPFRE	60
Dd	1	MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDSDNLSLFPFRE	60
Qy	61	PRSHFPPDLFPMCFPCGCYSRVVHCHSLGILTSVPTNIPDTRMLDLQNKKIKEIKEND	120
Dd	61	PRSHFPPDLFPMCFPCGCYSRVVHCHSLGILTSVPTNIPDTRMLDLQNKKIKEIKEND	120
Qy	121	FKGLTSLYGLLIINNKLTKTHPKAFLTTKKLRLLYLSHNOLSEIPLNPKSIAELRIHEN	180
Dd	121	FKGLTSLYGLLIINNKLTKTHPKAFLTTKKLRLLYLSHNQJSEIPLNPKSIAELRIHEN	180
Qy	181	KVKKIQTDFKGMMALHVLEMSANPLDNNGIEPGAFEGTVTFHIRIAEAKLTSPVKGLPP	240
Dd	181	KVKKIQTDFKGMMALHVLEMSANPLDNNGIEPGAFEGTVTFHIRIAEAKLTSPVKGLPP	240
Qy	241	TLLLEHLHDYNKISTIVELEDKFYKEIQRLQGLGNKKITDIENGSLANTPRVREIHLENNKL	300
Dd	241	TLLLEHLHDYNKISTIVELEDKFYKEIQRLQGLGNKKITDIENGSLANTPRVREIHLENNKL	300
Qy	301	KKIPSGLPPELKYLQIIFLHSNSTARVGVDFCPTVPKMKKSLYSAISLFNPNPKYHEMQP	360
Dd	301	KKIPSGLPPELKYLQIIFLHSNSTARVGVDFCPTVPKMKKSLYSAISLFNPNPKYHEMQP	360
Qy	361	ATFRCVLSRMVSQVLGNFGM 379	
Dd	361	ATFRCVLSRMVSQVLGNFGM 379	

RESULT 12
US-10-176-918-328
; Sequence 328, Application US/10176918
; Publication No. US2003002725A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 328
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-328

Query Match 100.0%; Score 1992; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 8.6e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDNSLFPPTRE 60
Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFPPTRE 60
Qy 61 PRSHFFPDLFPMCPGQCQYRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFPDLFPMCPGQCQYRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEIKEND 120
Qy 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNSQLSEIPLNPKSLAELRIHEN 180
Db 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNSQLSEIPLNPKSLAELRIHEN 180
Qy 181 KVKKIQKDTFGKMNALHVLMSANPLDNNNGIEPGAFEGTVFHIRIAEAKLTSVPKGLPP 240
Db 181 KVKKIQKDTFGKMNALHVLMSANPLDNNNGIEPGAFEGTVFHIRIAEAKLTSVPKGLPP 240
Qy 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKIIDTENGSLANIPRVREIHLNNKL 300
Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKIIDTENGSLANIPRVREIHLNNKL 300
Qy 301 KKIPSGLPKYLQIIFLHSNSTARVGNDFCPTVPKMKKSLYSALSIFNPNVYWMOP 360
Db 301 KKIPSGLPKYLQIIFLHSNSTARVGNDFCPTVPKMKKSLYSALSIFNPNVYWMOP 360
Qy 361 ATFRCVLSRMSVOLGNFGM 379
Db 361 ATFRCVLSRMSVOLGNFGM 379

RESULT 13
US-10-176-921-328
; Sequence 328, Application US/10176921
; Publication No. US2003002726A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 328
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-921-328

Query Match 100.0%; Score 1992; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 8.6e-159;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFPPTRE 60
Db 1 MKEYVLLFLALCSAKPFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFPPTRE 60
Qy 61 PRSHFFPDLFPMCPGQCQYRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEIKEND 120
Db 61 PRSHFFPDLFPMCPGQCQYRVVHCSDLGLTSVPTNIPEDTRMLDLQNNKIKEIKEND 120
Qy 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNSQLSEIPLNPKSLAELRIHEN 180
Db 121 FKGLTSLYGLILNNKLTTHPKAFLTTHKRLRLYLSHNSQLSEIPLNPKSLAELRIHEN 180
Qy 181 KVKKIQKDTFGKMNALHVLMSANPLDNNNGIEPGAFEGTVFHIRIAEAKLTSVPKGLPP 240
Db 181 KVKKIQKDTFGKMNALHVLMSANPLDNNNGIEPGAFEGTVFHIRIAEAKLTSVPKGLPP 240
Qy 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKIIDTENGSLANIPRVREIHLNNKL 300
Db 241 TLELHLDYNKISTVELEDFKRYKELQRLGLGNKIIDTENGSLANIPRVREIHLNNKL 300
Qy 301 KKIPSGLPKYLQIIFLHSNSTARVGNDFCPTVPKMKKSLYSALSIFNPNVYWMOP 360
Db 301 KKIPSGLPKYLQIIFLHSNSTARVGNDFCPTVPKMKKSLYSALSIFNPNVYWMOP 360
Qy 361 ATFRCVLSRMSVOLGNFGM 379
Db 361 ATFRCVLSRMSVOLGNFGM 379

RESULT 14
US-10-137-865-328
; Sequence 328, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

```

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 328
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-137-865-328

```

Query Match	100.0%	Score	992;	DB	9;	Length	379;
Best Local Similarity	100.0%;	Pred.	No. 8.6e-159;				
Matches	379;	Conservative	0;	Mismatches	0;	Indels	Gaps
QY	1	MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDNSLFPTRRE	60				
Ddb	1	MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDDDDNSLFPTRRE	60				
QY	61	PRSHFFPFDFPMCPFCQCQSYRWVHCSDLGTSVTNPFTDRLMDLQNKKIKEIKEND	120				
Ddb	61	PRSHFFPFDFPMCPFCQCQSYRWVHCSDLGTSVTNPFTDRLMDLQNKKIKEIKEND	120				
QY	121	FKGTLSYGLILNNNKUTKIHPKAFTTKKLRLRYLSHNQLSEIPLNLPKSIAELRIHEN	180				
Ddb	121	FKGTLSYGLILNNNKUTKIHPKAFTTKKLRLRYLSHNQLSEIPLNLPKSIAELRIHEN	180				
QY	181	KVKKIQKDTFKGMMNALHVLEWSANPDNGIEPGAEGVTVFHIARIAEAKLTSPVKGLPP	240				
Ddb	181	KVKKIQKDTFKGMMNALHVLEWSANPDNGIEPGAEGVTVFHIARIAEAKLTSPVKGLPP	240				
QY	241	TLELHLHDYNKISTVELEDPKRYKEIQRLGLGNKKTIDIENTSLANIPRVREIHLENKKL	300				
Ddb	241	TLELHLHDYNKISTVELEDPKRYKEIQRLGLGNKKTIDIENTSLANIPRVREIHLENKKL	300				
QY	301	KKIFSGIPPELYKLIQIIFLHSNSTARVCVNDFTPVPKMKKSLYSAISLFNNPVKYWEMQP	360				
Ddb	301	KKIFSGIPPELYKLIQIIFLHSNSTARVCVNDFTPVPKMKKSLYSAISLFNNPVKYWEMQP	360				

RESULT 15

US-10-140-474-328	Sequence 328, Application US/10140474
Publication No. US20030032156A1	GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.	APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura	APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen	APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.	APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.	APPLICANT: Gurney, Austin L.



94964

From:
Sent:
To:
Subject:

Li, Ruixiang
Friday, May 23, 2003 1:46 PM
STIC-Biotech/ChemLib
Sequence search of Application NO: 09/944,457

Please do:

(i) a standard search on SEQ ID NO: 2 against commercial amino acid databases;

(ii) a standard search on SEQ ID NO: 2 against pending interference amino acid databases, print out the summary table only, with 500 hits and no alignments.

Thank you very much!

Ruixiang Li
GAU 1646
CM1 10E18
Mail Box 10D19
306-0282

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

